U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

SEARCH REQUEST FORM

Requestor's Name:	· · · · · · · · · · · · · · · · · · ·	Serial Number:		
Date:	Phone:		Art Unit:	
Search Topic: Please write a detailed statement of sterms that may have a special meaning please attach a copy of the sequence.	ig. Give examples or releve	ent citations, authors, keyw	ords, etc., if known. For sequences,	
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	STAFF US	SE ONLY		
Date completed: Object of Comp		rch Site	Vendors	
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Total time: 2.8		N.A. Sequence	Geninfo	
Number of Searches:		A.A. Sequence	SDC	
Number of Databases:		Structure	DARC/Questel	
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PTO-1590 (9-90)

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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ALIGNMENTS

New low temperature expression chitinase gene for producing a plant grade highly resistant to psychophilic plant pathogenic microbes . Wheat; chitinase; low temperature expression; hardened; plant; snow mould resistance; psychophilic plant pathogen; barley. Wheat chitinase protein homologous to barley chitinase. AAB11487 standard; protein; 256 AA. (HOKK-) HOKKAIDO NOGYO SHIKENBACHO 99JP-0081694. 99JP-0081694. (first entry) WPI; 2001-027417/04. Triticum aestivum. JP2000270866-A. 25-MAR-1999; 25-MAR-1999; 02-MAR-2001 03-OCT-2000. AAB11487; AAB11487

Claim 1; Fig 1; 11pp; Japanese.

This invention describes novel wheat chitinase genes. The invention also describes a method for the isolation of a low temperature expression ${\sf c}$

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us-09-534-229c-1.rag

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chitinase gene in which the mRNA is extracted from a fully hardened autum wheat PII/3438 (of high snow mould resistance). The genes are useful for creating a plant grade, highly resistant to psychophilic plant pathogenic microbes.
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The present sequence is winter rye (Secale cereal L. cv. Muskateer)
(ETT46 preprotein. The mature protein, which is also claimed, is a chitinase-like protein that has chitinase (antifungal) and antifreeze activities. CHT46 cDNA (see AAXA4890) was obtained by isolating manh from rye plants grown at low temperatures in the absence of pathogens or other stresses, i.e. under conditions when only chitinases with antifreeze activity would be expressed in chitinases with antifreeze activity would be expressed in bacterial and yeast (Pichia) systems and in Arabidopsis thaliana. The chitinase-like antifreeze proteins can be used: to increase field survival of plants, animals and microorganisms; to increase field survival of plants, animals and microorganisms exposed to sub-zero temperatures; to inhibit ice recrystallisation in biological capterials or foods; for cryopreservation and hypothermic protection of cells, embryos, tissues etc. (particularly human platelets); and to cills, embryos, tissues etc. (particularly human platelets); and to diseases or spoilage caused by low temperature pathogens (particularly fungi) in plants, froze foods and any cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved by the percentage of the pathogens cryopreserved by the percentage of 
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\begin{array}{l} \texttt{E} \times \texttt{S} \times \texttt{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
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The present sequence is winter rye (Secale cereal L. cv. Muskateer)
CHT46 mature protein. It lacks the 22-amino acid signal peptide
of the preprotein (see AAM98081), which is also claimed. Mature
CHT46 is a chitinase-like protein that has chitinase (antifungal)
and antifreeze activities. CHT46 preprotein cDNA (see AAX24890) was
condained by isolating mRNA from rye plants grown at low temperatures
in the absence of pathogens or other stresses, i.e. under conditions
in the absence of pathogens or other stresses, i.e. under conditions
when only chitinases with antifreeze activity would be expressed in
bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.
CHT46 and CHT9 (see AAW98079-80) have been cloned and expressed in
bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.
CHT46 and CHT9 (see AAW98079-80) have been cloned and expressed in
bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.
CHT46 and CHT9 (see AAW98079-80) have been cloned and expressed in
bacterial and yeast (Pichia) systems and microcorganisms to increase field
survival of plants, animals and microcorganisms exposed to sub-zero
chemperatures; to inhibit ice recrystallisation and hypothermic protection
of cells, embryos, tissues etc. (particularly human platelets); and
progression of diseases or spoilage caused by low temperature
chypreserved biological material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGFIQLTGRSNYDLAGRAIGKD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPTAADTAAGRVPGYGVIT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding antifreeze polypeptides from plants -
particularly with chitinase activity, used to impart frost, and
pathogen, resistant to plants, for preservation of foods, cells etc.
and for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 VGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLAAFF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20; Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A maize chitinase polypeptide designated 2mCh15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1196; DB 20
Pred. No. 2e-110;
7; Mismatches 3
                                                                                                                             Moffatt B, Xiong F;
                                                                                                                                                                                                                                                                                                         Claim 10; Fig 22c; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB18903 standard; Protein; 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.8%;
95.6%;
                   98WO-CA00745
                                                     970S-0903872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.6
Matches 219; Conservative
                                                                                       (ICEB-) ICE BIOTECH INC
                                                                                                                            Hew C,
                                                                                                                                                            WPI; 1999-153795/13
                                                                                                                                                                               N-PSDB; AAX24890
                                                     31-JUL-1997;
                                                                                                                            Griffith M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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AAB18903
ID AAB1
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AC AAB1
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The present sequence represents a maize chitinase polypeptide. The prescrition describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18894, AAB18895, AAB188902-05), and glucosyl hydrolase family 18 chitinases (AAB18895, AAB189907-98 and AAB18900-01). The level of chitinase in plants can be modulated to enhance disease resistance in are also useful as molecular markers for genotype in a plant, and for sequence shuffling.
                                                                                                                                                                                                                                                                                                 New maize chitinase genes encoding seven chitinases of glucosyl hydrolase family 19 are useful for enhancing disease resistance in crop plants by modulating its expression in plants
             Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase famiy 18; pathogen control; disease resistance; molecular marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AISPPYYGRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 PSCHNVALRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGM 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 AFIAAANTFPGFGTTGSADDI-KRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MARFA--ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.8%; Score 992; DB 21; Length 252; 72.8%; Pred. No. 3.6e-90; ive 23; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tobacco endochitinase PR-Q precursor.
                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 85; 96pp; English.
                                                                                                                                                                                                 (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253
                                                                                                                                          2000WO-US06121.
                                                                                                                                                                       99US-0125915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR76714 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 LGTATGGNLDCYTQRNF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 lgvgygdnidcysgghf 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 72.8
Matches 187; Conservative
                                                                                                                                                                                                                               Yalpani N;
                                                                                                                                                                                                                                                        WPI; 2000-628269/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 AA;
                                                                                                                                                                                                                                                                         N-PSDB; AAA96231
                                                                                 WO200056908-A2.
                                                                                                                                          09-MAR-2000;
                                                                                                                                                                     24-MAR-1999;
                                                                                                                                                                                                                            Simmons CR,
                                                                                                              28-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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AAR76714
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pcht28 (AAQ93034) and pcht1 (AAQ93035), were derived from the leaves of drought-stressed L. chlease plants. The encoded chitlanses (AAR76712, AAR76713, respectively) may protect plants from pathogen attack during water stress. Recombinant chitinase was expressed in E. coli.
                                                                                                                                                                                                                                                                                                                                                    New endo:chitinase gene and protein - isolated from wild tomato
Lycopersicon chilense plants, having activity against plant pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 YYGRGPIQLTGRSNYDLAGRAL--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 AANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 RFAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endochitinase; wild tomato; osmotic stress; abscisic acid; drought;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 Osmotic stress and ABA-responsive endochitinase cDNA clones,
water stress; class II chitinase; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 822.5; DB 16;
Pred. No. 2.2e-73;
2; Mismatches 60;
                                                         Location/Qualifiers
1..24
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 24-25; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wild tomato endochitinase pchtI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR76713 standard; Protein; 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 60.4%;
Local Similarity 61.2%;
Nes 156; Conservative 33
                                                                                                                                                                                                                                                                            Ϋ́ц
                                                                                                                                                                                  93CA-2110764
                                                                                                                                                                                                             93CA-2110764
                                Lycopersicon chilense Dun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || |||| |:|||
ptgenldcnnqknfa 251
                                                                                                                                                                                                                                                                            Ζ,
                                                                                                                                                                                                                                            (TABA/) TABAEIZADEH Z.
                                                                                                                                                                                                                                                                            Tabaeizadeh
                                                                                                                                                                                                                                                                                                       WPI; 1995-269746/36.
N-PSDB; AAQ93034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 AA;
                                                                                                                                                                                  06-DEC-1993;
                                                                                                                                                                                                             06-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-1995
                                                                                                                      CA2110764-A
                                                                                                                                                   07-JUN-1995
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                                                                         Peptide
                                                                                                                                                                                                                                                                          Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                         New endo:chitinase gene and protein - isolated from wild romato
Lycopersicon chilense plants, having activity against plant pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 TFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sfpgfgttgddtarrkelaaffgqtshettggsl-saepftggycfvrqndq--sdryyg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVAL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGXYTRYCGMLGTATGGN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 alfccvfflflt----gsladgigsivtsdlfnemlknrndgrcpangfytydafiaaan 64
         tomato; osmotic stress; abscisic acid; drought; II chitinase; Lycoperison chilense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endochitinase; wild tomato; osmotic stress; abscisic acid; drought;
                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding an osmotic stress and ABA-responsive endochitinase was derived from the leaves of drought-stressed L. chilense plants. The encoded chitinase (AAR76712) shared 78% identity with that of chitinase class II isoform PR-Q of tobacco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.2%; Score 846.5; DB 16; 63.9%; Pred. No. 9.4e-76; iive 32; Mismatches 51;
                                                                                                  1..24
/label= Sig_peptide
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 27; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR76712
ID AAR76712 standard; Protein; 253
                                                                                                                                                                                                                                                                                                  Ľ,
                                                                                                                                                                                                        93CA-2110764
                                                                                                                                                                                                                                    93CA-2110764.
                                                                                                                                                                                                                                                                                                    Ϋ́ц
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wild tomato endochitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                 Tabaeizadeh Z,
        , wild class
                                                                                                                                                                                                                                                                 (TABA/) TABAEIZADEH
                                                                                                                                                                                                                                                                                                                            WPI; 1995-269746/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 159; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 LDCYTQRNF 254
                                                     Nicotiana tabacum
      Endochitinase;
                                                                                                                                                                                                                                    06-DEC-1993;
                                                                                                                                           CA2110764-A
                                                                                                                                                                        07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR76712;
                                                                                                Peptide
                                                                                                                                                                                                                                                                                               В,
                      water
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Length 253;

61

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128 PIQLIGRSNYDLAGRALGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLD
                                                                                                                                                                                                                                                                                                         This sequence was deduced from a P.hybrida cDNA sequence having 80 per cent homology with tobacco clone PROB30 which encodes extracellular chitinase PR-Protein R. The gene can be inserted into an appropriate plasmid for production of transgenic plants having resistance to fungal pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular chitinase; antifungal; transgenic plant; synergism; beta-1,3-glucanase gene.
                                                                                                                                                                                                                                          Plants with improved resistance to pathogenic fungi - othitinase and/or beta-1,3-glucanase genes modified for over-expression targetted to apoplasts
                                                                                                                                                                   Van Bol
                                                                                                                                                                                                                                                                                                                                                                                                                                         59.8%; Score 814.5; DB 12;
62.1%; Pred. No. 1.4e-72;
iive 31; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petunia hybrida extracellular chitinase protein
                                                                                                                                                                   Meulenhoff EJ,
Woloshuk CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW31296 standard; Protein; 254 AA.
                                                                                                                                                                                                                                                                                           Example 4; Fig 1; 55pp; English.
                                                                                                                                                                                Vloemans AA,
                                                                                                                                                                    Melchers LS,
                                                                                 91EP-0200191.
                                                                                                        90NL-0000222
                                                                                                                               MOGEN INT NV.
RIJKSUNIV TE LEIDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                          WPI: 1991-232019/32
                                                                                                                                                                                                                                                                                                                                                                                                        254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 cyndrnfa 252
                                                                                                                                                                                 Sela-Buurlage MB,
                                                                                                                                                                                                                     N-PSDB; AAQ12897
           Petunia hybrida
                                                                                                                                                                       Cornelissen BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LI-MAR-1998
                                                                                  30-JAN-1991;
                                                                                                         30-JAN-1990;
                                                         07 -AUG-1991
                                  EP440304-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S:
Matches 154,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW31296;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                    MOGE-)
                                                                                                                                                (UXLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW31296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q_{Y}
3;
                                                                                                                                                                                                                                                                                                                                            2 Osmotic stress and ABA-responsive endochitinase cDNA clones, pcht28 (AAQ93034) and pcht1 (AAQ93035), were derived from the leaves of drought-stressed L. chilense plants. The encoded chitinases (AAR76712, AAR76713, respectively) may protect plants from pathogen attack during water stress. Recombinant chitinase was expressed in E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRW 188
                                                                                                                                                                                                                                                                                                Lycopersicon chilense plants, having activity against plant pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gttgddtarkkeiaaffgqtshetnggsagt---ftggycfvrqidq--sdryygrgpiq 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 AAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 TPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                    New endo: chitinase gene and protein - isolated from wild tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.9%; Score 816.5; DB 16; Length 250;
.larity 62.3%; Pred. No. 8.7e-73;
Conservative 30; Mismatches 56; Indels 7;
  water stress; class II chitinase; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR13274 standard; Protein; 254 AA
                                                Location/Qualifiers
1..21
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                          Claim 2; Page 26-27; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fungal resistance; phytopathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Petunia extracellular chitinase.
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                                                                                                                                                                                                                            Ϋ́
                                                                                                                                                 93CA-2110764
                                                                                                                                                                          93CA-2110764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                         Lycopersicon chilense Dun.
                                                                                                                                                                                                                            Tabaeizadeh
                                                                                                                                                                                                                                                   WPI; 1995-269746/36.
                                                                                                                                                                                                   (TABA/) TABAEIZADEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
hes 154; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                         250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nngknfa 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 YTQRNFA 255
                                                                                                                                                                                                                                                               N-PSDB; AA093035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-0CT-1991
                                                                                                                                                    06-DEC-1993;
                                                                                                                                                                           06-DEC-1993;
                                                                                                   CA2110764-A
                                                                                                                           07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR13274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                           Chen R,
                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
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AAR13274
ID AAR1
XX
AC AAR1
XX
DT 14-0
XX
XX
XX
XX
XX
XX
XX
KW fung
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      qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qγ
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Gaps

7;

Indels

Length 254;

contains

JS;

Roekel . JF;

247

us-09-534-229c-1.rag

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Vloemans AA,
                                                                                                                                                                                     18-FEB-1997;
                                                                                                                                                                                                        19-APR-1993;
                          20-0CT-2000
                                                                                                                                                                                                                  29-JAN-1991;
                                                                                                                                               US6087560-A.
                                                                                                                                                                  11-JUL-2000
                                                                                                                                                                                                                                                               Cornelissen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
        AAB07512;
                                                                                                                                                                                                                                  (UYLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
                                                                                                                                                                                                                                             (MOGE-)
                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
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                                                                                                                                                                                                                                                                                                This sequence represents an extracellular chitinase which is used to construct a transgenic plant in a novel method to produce plants resistant to fungal attack. Such transgenic plants expressing an intracellular plant chitinase gene and a plant beta-1,3-glucanase gene within its tissues are predicted to exhibit improved resistance to pathogenic fungi. Such genes should be operably linked to promoters and terminators and optionally a gene encoding a selectable or screenable trait. Plants that overexpress the chitinase and glucanase gene exhibit a synergistic antifungal effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AVCAAALLLAVAAGGAAAQGVGSVITTRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                     Fungus-resistant transgenic plants - containing genes encoding intracellular chitinase and beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 18; Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                      ĽS;
                                                                                                                                                                                   Bol JF, Cornelissen BJC, Linthorst HJM, Melchers
Meulenhoff EJS, Sela-buurlage MB, Van ROEKEL JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
                                   1..23
/label- signal_peptide
24..24 /note= "extracellular chitinase"
                                                                                                                                                                                                                                                                                                                                                                                                                         59.8%; Score 814.5; DB 1 62.1%; Pred. No. 1.4e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB07512
ID AAB07512 standard; Protein; 254 AA.
                           Location/Qualifiers
                                                                                                                                                                                                                                                                               Example 4; Fig 1; 42pp; English.
                                                                                                                     93US-0047413
                                                                                                                                      91US-0647831
                                                                                                                                                                                             EJS, Sela-Duur.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.18
Matches 154; Conservative
                                                                                                                                                         NV.
LEIDEN.
                                                                                                                                                                                                                        WPI; 1997-479536/44.
                                                                                                                                                        MOGEN INT I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 CYTQRNFA 255
                                                                                                                                                                                                                                  N-PSDB; AAT89951
       Petunia hybrida
                                                                                                                                                                                                                                                                                                                                                                                                254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vloemans AA,
                                                                                                                     19-APR-1993;
                                                                                                                                      29-JAN-1991;
                                                                               US5670706-A.
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                   Peptide
                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
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The present sequence represents an extracellular chitinase. The specification describes transgenic plants which express a chitinase gene and a glucanase gene. The expression of the chitinase and beta-1,3-glucanase genes produces an antifungal effect. The transgenic plants are useful for improving plant resistance to pathogenic fungi. The recombinant polynucleotides and the process are useful for producing fungal resistant plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New transgenic plants expressing chitinase and glucanase have improved resistance against pathogenic fungi, particularly against Alternaria alternata or Fusarium oxysporum f. sp. lycopersici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meulenhoff EJS, Sela-buurlage MB;
JF, Linthorst HJM, Van Roekel JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 WIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 254;
                                                                                            Chitinase; transgenic plant; beta-1,3-glucanase; antifungal; plant resistance; pathogenic fungi; fungal resistant plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                           Amino acid sequence of an extracellular chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .4e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.8%; Score 814.5; 62.1%; Pred. No. 1.4
                                                                                                                                                                                                                                                                          /note= "signal peptide"
                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LS,
Bol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0647831.
                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0801563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0047413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Melchers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Woloshuk CP,
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ķ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-498214/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOGEN INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 CYTORNEA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAA58909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BJC,
                                                                                                                                                                           Petunia hybrida
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∺;

Tue

245 cyngrnfa 252

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This invention describes novel wheat chitinase genes. The invention also describes a method for the isolation of a low temperature expression chitinase gene in which the mRNA is extracted from a fully hardened autumn wheat PII73438 (of high snow mould resistance). The genes are useful for creating a plant grade, highly resistant to psychophilic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----YY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRIAMWFWMTAQGNKPSCHNVA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 GAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKR 81
                                                                                                                                                                                                                                                                                                                                                                      low temperature expression chitinase gene for producing a plant te highly resistant to psychophilic plant pathogenic microbes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wheat; chitinase; low temperature expression; hardened; plant; snow mould resistance; psychophilic plant pathogen; rye.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.6%; Score 798; DB 22; Length 323; 59.6%; Pred. No. 8.3e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                        Wheat chitinase protein homologous to rye chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISKATSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR52577 standard; Protein; 266 AA.
                       AAB11488 standard; protein; 323 AA.
                                                                                                                                                                                                                                                                                                               (HOKK-) HOKKAIDO NOGYO SHIKENBACHO
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Fig 2; 11pp; Japanese.
                                                                                                                                                                                                                                                           99JP-0081694
                                                                                                                                                                                                                                                                                       99JP-0081694
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                         WPI; 2001-027417/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 nldcynglsf 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathogenic microbes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 NLDCYTQRNF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                         Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 AA;
                                                                                                                                                                                                     JP2000270866-A.
                                                                                                                                                                                                                                                          25-MAR-1999;
                                                                                                                                                                                                                                                                                     25-MAR-1999;
                                                                               02-MAR-2001
                                                                                                                                                                                                                              03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Sim
les 149;
                                                   AAB11488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                grade
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR52577
ID AAR5
                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QΫ́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
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Gaps

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Chitinase is an enzyme which breaks down chitin, the major protein in insect exoskeletons. The coding sequence may be used in the construction of transgenic organisms, especially plants, to produce pathogen resistan organisms. The genome of such transgenic organisms preferably contains more than one gene with pathogen inhibiting activity, each gene under the control of active promoters. The two gene products then show a synergistic increase in pathogen induced activity so that the transgenic organisms have a greater degree of resistance or resistance against a wider spectrum of diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 -----ATSPPYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWM 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                Transgenic organisms contg. at least 2 pathogen inhibiting genes - esp. plants contg. genes with antifungal activity, show synergistic increase in disease resistance, also new DNA transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 TAQGNKPSCHNVALRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 TFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK-----
                                                                                                 Antifungal, pathogen; resistance; transgenic organism; synergy; crop protection; transgenic plant; chitinase; glucanase; protein synthesis inhibitor; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                             Jach G, Logemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
                                                                                                                                                                                                                                                                                                               (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.7%; Score 772; DB 15; 56.8%; Pred. No. 2.4e-68; tive 31; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 13-14; 19pp; German
                                                                                                                                                                                                                                                                                                                                           Eckes P, Gornhardt B, Schellj, Goernhardt B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 krycdilgvgygnnldcysgrpfa 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 TRYCGMLGTATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                  92DE-4234131.
                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-136599/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 AA;
                                                                                                                                                               Hordeum vulgare L.
                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ62518
                                                                                                                                                                                                                                                    09-OCT-1992;
                                                                                                                                                                                                                                                                                  09-OCT-1992;
                                        05-DEC-1994
                                                                        Chitinase G.
                                                                                                                                                                                           DE4234131-A
                                                                                                                                                                                                                         21-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150;
                                                                                                                                                                                                                                                                                                                                          Chet I, 1
Mundy J,
              AAR52577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the pumpkin chitinase. Chitinase is an enzyme decomposing chitin (not present in plant cell membranes) found in the cell membranes of fungi. Plants have this enzyme to protect themselves from being infected with pathogenic fungi, and the chitinase gene can be introduced into plants to improve their resistance to diseases caused by fungi. As the amino acid sequence of the chitinase does not have any region to be cleaved by ubiquitous peptidases in cells, the chitinase produced by genetic recombination technology works for various host cells and serves for plant immunity to confer disease resistance on plants as
                                                                                                                                  pumpkin; enzyme; decompose; plant cell membrane; peptidase;
. membrane; pathogenic fungus; disease resistance; chitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 ggggggsvgsiinealynqmlkyskdprcpsngfyrynafitaaqsfsgfgttgdaatrk 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ATSPPYYGRG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYIRYCGMLGTATGGNLD
                                                                                                                                                                                                                                                                                                                                                                                          Chitinase derived from pumpkin - used to protect plants against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 756.5; DB 18;
Pred. No. 9.4e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                          (NIHA ) JAPAN ENERGY CORP.
(SEKI-) ZH SEKIYU SANGYO KASSEIKA CENTER.
                      AAW24554 standard; Protein; 292 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 2; 36pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.5%; Scc
58.3%; Pre
tive 26;
                                                                                                                                                                                                                                                        95JP-0347367
                                                                                                                                                                                                                                                                                 95JP-0347367
                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT79940, AAT79941
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144; Conservative
                                                                                                                                                                                                                                                                                                                                                   1997-380170/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ||:|
cnngrsf 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTORNF 254
                                                                                                                                                                                                                                                                                                                                                                                                         pathogenic fungi
                                                                                                                                                                       Cucurbita pepo.
                                                                                                                                                                                                JP09163987-A.
                                                                                                                                                                                                                                                        14-DEC-1995;
                                                                                                                                                                                                                                                                                 14-DEC-1995;
                                                                            10-OCT-1997
                                                                                                                                                fungal cell
                                                                                                                                                                                                                             24-JUN-1997.
                                                                                                                               Chitinase;
                                                 AAW24554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
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The sequence given is encoded by the rice chitinase gene. The promoter region of this gene (see AAQ31407) is responsive to physical and/or biological stress. The pattern of expression of this protein in mature plants is characteristic. There is a low level of expression in leaves, a moderate level in plant stems and the highest level in roots and the male and female parts of the plant. The chitinase promoter sequence may be linked to a reporter gene for expression in monor or dicoryledon plants. Expression of this reporter gene may be used to study patterns of development and controlled expression of plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---AISPPYY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRGFIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 AGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDI 79
                                                                                                                                                                                                                                                            /note= "Region conserved between class I and class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||::||| |||||||||| | | : ||||||||
krevaaflagtshettggwatapdgpytwgycfkeenggagpdycggsagwpcaagkkyy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is
in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chitinase; physical; biological; stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA fragment contg. chitinase gene and its regulatory region responsive to mature plant stress and has low level expression leaves, moderate level expression in stem and high level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 336;
                                                                                                                                                    leaves; stems; roots; male; female; reporter; monocotyledon; dicotyledon; development; plant; defence; selectable; genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 KRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 747.5; DB 1
Pred. No. 8.8e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                         II chitinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 33-34; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                            Location/Qualifiers
123..323
              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        defence genes and selectable genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.9%; Scor
57.3%; Pred
tive 28; 1
            standard; Protein; 336
                                                                                                                                                                                                                                                                                                                                                                     92WO-US04282
                                                                                                                                                                                                                                                                                                                                                                                                  91US-0704288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 142; Conservative
                                                                                                     RCH10 chitinase protein
                                                                                                                                     Promoter; region; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-415785/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression in roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhu Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ31407
                                                                                                                                                                                                 Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                  22-MAY-1991;
                                                                      20-APR-1993
                                                                                                                                                                                                                                                                                                                                                                   21-MAY-1992;
                                                                                                                                                                                                                                                                                                         WO9220807-A.
                                                                                                                                                                                                                                                                                                                                     26-NOV-1992.
           AAR29019
                                         AAR29019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lamb CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                               Key
Reqion
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AAR29019
                                                        δ
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Search completed: May
Job time: 7548 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 GRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCHNVA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AGGAAAQGVGSVIIRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDI 79
190 grgpiglsynfnygpaggaigadllgdpdlvasdatvsfdtafwfwmtpgspkpscnava 249
                          185 LRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGG 244
                                        54.9%; Score 747.5; DB 16; Length 336; llarity 57.3%; Pred. No. 8.8e-66; Conservative 28; Mismatches 63; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic plants contg. several plant defence associated proteins - have increased resistance to plant pathogens when grown in crops as a food source
                                                                                                                                                                                                                                                                              Chitinase; transgenic plant; disease resistance; crop improvement; tobacco; Nicotiana tabacum; plant defense; fungus pathogen; Cercospora nicotinae; Thanatephorus cucumeris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 KRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maher EA, Zhu Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 31-32; 45pp; English.
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                                                                                                                                                                          AAR67969 standard; Protein; 336 AA.
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N-PSDB; AAQ81346.
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Best Local Similarity
Matches 142; Conserv
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                                                                                 245 NLDCYTQR 252
                                                                                                        310 nidcysqr 317
                                                                                                                                                                                                                                                       Rice chitinase.
                                                                                                                                                                                                                                                                                                                                                  Oryza sativa.
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185 LRRWIPTAADTAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGG 244
                                                                245 NLDCYTOR 252
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72.518 Million cell updates/sec
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
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                                          Compugen Ltd
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US-08-229-050-9
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                       GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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No.
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TITLE OF INVENTION: A novel endochitinase gene
TITLE OF INVENTION: induced by osmotic stress and abscisic acid isolated
TITLE OF INVENTION: from the wild tomato Lycopersicon chilense Dun.
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                     Sequence 7, 1
Sequence 6, 1
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Sequence 35, Sequence 25, 2
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                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUDICESEE: CUSHMAN, DAKRI & CUSHMAN
STREET: 1100 New York Avenue, N.W., 9th Floor
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 720 kb diskette
COMPUTER: IBM PS/2, Model 30
COMPUTER: IBM PS/2, Model 30
COMPUTER: IBM PS/2, Model 30
COMPUTER: DEM PS/2, MODER
APPLICATION NUMBER: US/08/162,475A
FILING DATE: December 7, 1993
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.2%; Score 846.5; DB 1;
63.9%; Pred. No. 4.5e-82;
live 32; Mismatches 51;
US-08-379-259-8
US-07-704-288C-6
US-08-379-259-6
US-08-379-259-7
US-08-379-259-7
US-08-379-259-7
US-08-379-259-7
US-07-791-931-8
US-07-791-931-8
US-07-791-931-8
US-08-329-799-35
US-09-329-799-35
US-09-329-799-35
US-09-329-799-35
US-09-329-799-35
US-09-31-814-100
US-09-413-814-100
US-08-460-269-6
US-08-547-6
US-08-540-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: White, Paul E. Jr.
REGISTRATION NOMER: 321.
REFERENCE/DOCKET NUMBER: PEW/3122/204351
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: Protein ORIGINAL SOURCE: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-162-475A-5
; Sequence 5, Application US/08162475A
: Pattent No. 5656474
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 63.9
mes 159; Conservative
       unknown
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amino acid
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                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08162475A
Patent No. 555647
GENERAL INFORMATION:
APPLICANT: Zohreh Tabaeizadeh
TITLE OF INVENTION: A novel endochitinase gene
TITLE OF INVENTION: induced by osmotic stress and abscisic acid isolated
TITLE OF INVENTION: from the wild tomato Lycopersicon chilense Dun.
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                                                                                                                           186 RRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEBISKATSPPYYG 125
                  SFPGFGTTGDDTARRKELAAFFGQTSHETTGGSL-SAEPFTGGXCFVRQNDQ--SDRXKG 121
                                                               RGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVAL 185
                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.8%; Score 828.5; DB 1; Length 253; 61.6%; Pred. No. 3.7e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: CUSHMAN, DARBY & CUSHMAN 1100 New York Avenue, N.W., 9th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: December 7, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, Paul B. Jr.
REGISTRATION NUMBER: 32011
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MIDIUM TYPE: 3.5 inch, 720 kb diskette
COMPUTER: IBM PS/2, Model 30
OPERATING SYSTEM: PC-DOS 3.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   December 7, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 861-3000
TELEPAX: (202) 822-0944
INFORMATION FOR SEC ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: fro
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C. COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                                                                                                                                                            242 LDCYNQRNF 250
                                                                                                                                                                                               246 LDCYTORNF 254
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                                                                                                                                                                                                                                                                              RESULT 2
US-08-162-475A-2
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CITY: Wa
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TITLE OF INVENTION: A novel endochitinase gene
TITLE OF INVENTION: induced by osmotic stress and abscisic acid isolated
TITLE OF INVENTION: from the wild tomato Lycopersicon chilense Dun.
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIGRSNYDLAGRAI --GKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCHNVALRRW 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 GTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 GTTGDDTARKKEIAAFFGQTSHEINGGSAGT---FTGGYCFVRQIDQ--SDRYYGRGPIQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 YYGRGPIQLTGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                              11 AAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1100 New York Avenue, N.W., 9th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.9%; Score 816.5; DB 1
62.3%; Pred. No. 6.8e-79;
iive 30; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATORNEX/AGENT INFORMATION:
NAME: White, Paul E. Jr.
REFERENCE/DOCKET NUMBER: 32011
REFERENCE/DOCKET NUMBER: PEW/3122/204351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
COUNTRY: U.S.A.
ZID: 20005-518
ZIP: ZOND-518
COMPUTER REALABLE FORM:
TYPE: 3.5 inch, 720 kb diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Protein ORIGINAL SOURCE: Lycopersicon chilense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/162,475A
                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08162475A; Patent No. 5656474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PS/2, Model 30
OPERATING SYSTEM: PC-DOS 3.30
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              December 7, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 59.9%
Best Local Similarity 62.33
Matches 154; Conservative
                                                                                                                                                                                                  241 ATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                               237 PTGENLDCNNQKNFA 251
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APPLICANT: Cornelissen, Bernardus J.C.
APPLICANT: Melchers, Leo S.
APPLICANT: Melchenoff, Elisabeth J.S.
APPLICANT: Melchenoff, Elisabeth J.S.
APPLICANT: Van Roekel, Jeroen S.C.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Moloshuk, Charles P.
APPLICANT: Litthorst, Hubertus J.M.
APPLICANT: Litthorst, Hubertus J.M.
TITLE OF INVENTION: CORTAINING FUNGAL RESISTANT PLANTS, PROCESS FOR TITLE OF INVENTION: POLYNOCLES FOR USE THEREIN
MINDER OF INVENTION: POLYNOCLEOTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTF 67
            PIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCHNVALRR 187
                                                                   125 PIQLIGGSNYDLAGKALEQDLVNNPDLVATDATVSFKTAIWFWMTPQGNKPSCHDVITGR
                                                                                                                             WIPTAADIAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLD
                                                                                                                                                               Length 254;
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.8%; Score 814.5; DB 62.1%; Pred. No. 1.1e-78
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APPLICATION NUMBER: US/08/229,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/647,831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application \ensuremath{\text{US}}/08229050 Patent No. 6066491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Murashige, Kate H. REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 7575

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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California
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Matches 154; Conserv
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                                                                                                                                                                                                                                                           248 CYTQRNFA 255
                                                                                                                                                                                                                                                                                                                  245 CYNORNEA 252
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US-08-229-050-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Pa.
STATE: Ca.
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-08-229-050-9
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                        128 1
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APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: PUNGAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AVCABALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTF 67
Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE PATENTING STATEM.
SOFTWARE PATENTING STATEM.
SOFTWARE PATENTING Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,413
FILING DATE: 19-APR-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTORNEY-AGENT INFORMATION:
NAME: MUTANING NUMBER: ARTER IN NUMBER: MUTANING NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.8%; Score 814.5; DB 1; 62.1%; Pred. No. 1.1e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 24615-20022.00 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        Cornelissen, Bernardus J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sela-Buurlage, Marianne B.
Vloemans, Alexandra A.
Woloshuk, Charles P.
                                                                                                                                                                                                                                                                                                                                                                                                                    Melchers, Leo S.
Meulenhoff, Elisabeth J.S.
van Roekel, Jeroen S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Morrison & Foerster 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08047413 Patent No. 5670706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 59.8%
Best Local Similarity 62.1%
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-047-413-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Corneli,
APPLICANT: Melcher:
APPLICANT: Weulenh
APPLICANT: van Roel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94304-1018
                                                                                                                                                         242 NNOKNFA 248
                                                                                              249 YTORNFA 255
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STREET: 75
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                    US-08-047-413-9
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US-08-801-563-9
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APPLICANT: Melchers, Leo S.
APPLICANT: Walelenhoff, Elisabeth J.S.
APPLICANT: van Roekel, Jercem S.C.
APPLICANT: Sela-Buurlage, Marianne B.
APPLICANT: Moloshuk, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Mithorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             185 WIPSAADTSANRYPGYGVITNIINGGIECGKGQNARVEDRIGYYRRNVSIMNVAPGDNLD 244
                                                                      PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKBEISKATSPPYYGRG 127
                                                                                                                 128 PIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRR 187
                                                                                                                                                                                    188 WIPTAADIAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYYIRYCGMLGTATGGNLD
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/801,563 APPLICATION NUMBER: US/08/801,563 CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/047,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19-APR-1993
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-AN-1991
ATTORNEY AGENT INFORMATION:
NAME: MITCAShige, Kate H.
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                       Cornelissen, Bernardus J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Morrison & Foerster STREET: 755 Page Mill Road CITY: Palo Alto STATE: California COUNTX: USA ZIP: 94304-1018 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08801563 Patent No. 6087560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Cornel
                                                                                                                                                                                                                                                                                    245 CYNORNEA 252
                                                                                                                                                                                                                                                      248 CYTQRNFA 255
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66 FPGFGISGDDIARRKEIAAFFGQISHEIIGGSL-SAEPFIGGYCFVRQNDO--SDRYYGR 122
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                                                                                                                                                                                                                                                                                                    125 PIQLTGQSNYDLAGKAIEQDLVNNPDLVATDATVSFKTAIWFWMTPQGNKPSCHDVITGR 184
                                             Gaps
                                                                                                                                                                          68 PGFGTTGSADDIKKDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRG 127
                                                                                                                                                                                                     WTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLD 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANT 66
                                                                                  8 AVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LFCCVFFLFLT----GSLAQGIGSIVINDLFNEMLKNRNDGRCPANGFYTYDAFIAAANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 FPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 RWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 SVLALSEVVFLFLTGTLAQNVGSIVTSDLFDQMLKNRNDARCFAVRFYTYDAFIAAANSF
                                                                                                                                                                                                                                                                 PIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRR
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  Length 254;
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                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.4%; Score 808.5; DB 4;
61.0%; Pred. No. 4.9e-78;
iive 34; Mismatches 56;
59.8%; Score 814.5; DB 3;
62.1%; Pred. No. 1.1e-78;
iive 31; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: RAIKHEI, NALASHA V.
TITLE OF INVENTION: Nettle Lectin CDNA
FILE REFERENCE: MSO 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-07-791-931-9
; Sequence 9, Application US/07791931C
; Patent No. 6133507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Nicotiana tabacum
US-07-791-931-9
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                                                  Conservative
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Matches 152; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYNORNEA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                           248 CYTORNFA 255
      Query Match
Best Local Simi
Matches 154;
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Query Match 56.7%; Score 772; DB Best Local Similarity 56.8%; Pred. No. 4e-7 Matches 150; Conservative 31; Mismatches
FILE REFERENCE: MSU 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 266
TYPE: PRI
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FILING DATE: AUGUST 24, 1998
ANDER AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09138873A Patent No. 6271438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 KRYCDILGVGYGNNLDCYSQRPFA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 TRYCGMLGTATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 408-2500
TELERAX: (212) 765-2519
TELER: 238555
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARRACTERISTICS:
LENGTH: 266 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Baker & Botts
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 18,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kole, Lisa
REGISTRATION NUMBER: 35,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: A2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                               ; ORGANISM: Hordeum vulgare US-07-791-931-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tenser, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Tre
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
: New York
RY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-138-873A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ATSPPYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWM 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 SAQWPCAPGKRYYGRGPIQLSHNYNGPAGRAIGVDLLANPDLVATDATVGFKTAIWFWM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAQGNKPSCHNVALRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic pathogen-resistant organism
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56.8%; Pred. No. 4e-74;
Live 31; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                           TITLE OF INVENTION: Transgenic pathogen-resistant or
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: KOLE, LISA
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: A29542 FWC - 37/31335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEPHONE: (212) 765-2519
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%30.21.

%30.20.7.91-931-10

%30.20.7.91-931C

%30.20.7.9
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FILING DATE:
ATTONEX/AGENT INFORMATION:
NAME: Tenser, Arthur
REGISTRATION NUMBER: 18,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 KRYCDILGVGYGNNLDCXSQRPFA 266
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                                            Sequence 10, Application US/08812025 Patent No. 5804184 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 238555
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
TENGTH: 266 amt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 56.8%
Matches 150; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-812-025-10
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                  New York
U.S.A.
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STATE: New York
COUNTRY: U.S.A.
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172 TAQGNKPSCHNVALRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYY 231
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                                                                            6 ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                      66 TFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transgenic pathogen-resistant organism
12
; DB 4; Length 266;
4e-74;
ches 69; Indels
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RY: U.S.A.
90071-2921
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US-08-093-372-2
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                                            Matches 142;
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             Query Match
                                Local
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                                                                                                                                                                                                                                                                          118 -----ATSPPYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWM 171
                                                                                                                                                                                                                                                                                                                                                 172 TAQGNKPSCHNVALRRWIPTAADIAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYY 231
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY TITLE OF INVENTION: ELEMENTS
                                                                                                  Ouery Match 56.7%; Score 772; DB 4; Length 266; Best Local Similarity 56.8%; Pred. No. 4e-74; Matches 150; Conservative 31; Mismatches 69; Indels 14; Gaps
                                                                                                                                                                                                    3 SLAVVVAVVATVAMAIGTARGSVSSIVSRAQFDRMLLHRNDGACQAKGFYTYDAFVAAAA 62
                                                                                                                                                                               6 ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: PRETIY, SCHROEDER, BRUEGGENANN & CLARK
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 TRYCGMLGTATGGNLDCYTQRNFA 255
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APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
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TELEFAX: (619) 546-9392
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                              MOLECULE TYPE: protein
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amino acid
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                                                  US-09-138-873A-10
             TOPOLOGY:
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                                                                                                                                                                                                                                               125 GRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVA 184
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                                                                              20 AGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDI 79
                                          Gaps
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Length 336;
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Patent No. 5530187
GENERAL INFORMATION:
APPLICANT: Lamb, Christopher J.
APPLICANT: Lamb, Christopher J.
APPLICANT: Maher, Eileen A.
APPLICANT: Dixon, Richard A.
TITLE OF INVENTION: TRANSGENCE GENES
TITLE OF INVENTION: DISEASE RESISTANCE GENES
NUMBER OF SEQUENCES: 4
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                                          Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,372
FILING DATE: 16-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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  54.9%; Score 747.5; DB 1; 57.3%; Pred. No. 2.2e-71; iive 28; Mismatches 63;
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57.3%; Pred. No. 2.2e-71;
tive 28; Mismatches 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pretty, Schroeder, Brueggemann & STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31,192
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TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 336 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-093-372-2
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Best Local Similarity
Matches 142; Conserva
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63 APIDLSALISRSTEDQMLKHRNDGACPAKGEYIYDAFIAAAKAYPSFGNTGDTATRKREI 122
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APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: LAMB, CHRISTOPHER J.
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: PRETIY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 AAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDL 83
                                                                                                                                                                         125 GRGPIQLFGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNXPSCHNVA 184
                                                                                                                                                                                                                             185 LREWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGG 244
                                                                                                                                                                                                                                                 -ATSPPYY 124
20 AGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDI 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: #800
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53.9%; Pred. No. 2.2e-68;
Live 37; Mismatches 64
                                                                              80 KRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4337
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/07704288C Patent No. 5399680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
COUNTRY: United States
ZIP: 90071-2921
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STATE: California
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Best Local Similarity
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310 NLDCXSQR 317
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                                                                                                                                                                                                           185 LRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGG 244
                                                                                                                                                                                                                                                                                   Gaps
                                                      -ATSPPYY 124
                              20 AGGAAAQGVGSVIIRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTIGSADDI 79
                                                                                                                                  15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK STREET: 444 South Flower Street, Suite 2000 CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08379259
Patent No. 5695939
GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: LEEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.9%; Score 747.5; DB 1; 57.3%; Pred. No. 2.2e-71; ative 28; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                          80 KRDLAAFFGQTSHETFGGTRGAAD-QFQWGYCFKEEISK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY AGENT INFORMATION:
NAME: Reiter Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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(619) 546-9392
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Best Local Similarity 57.33
Matches 142; Conservative
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                    132 IGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPT 191
                                                                                                                                                                        243 SADVAARRLPGYGTVTNIINGGLECGRGQDSRVQDRIGFFKRYCDLLGVGYGNNLDCYSQ 302
-----SPPYYGRGPIQL 131
                                                                                                 SWNYNYGQCGRAIGVDLLNKPDLVAIDSVISFKSALWFWMTAQSFKPSSHDVITSRWTPS
                                                                                                                                                    192 AADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQ
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COUNTRY: United States
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RE-BASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: 2HU, QUN
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: BLEBNIS
TITLE OF INVENTION: BLEBNIS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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53.9%; Pred. No. 2.2e-68;
tive 37; Mismatches 64,
84 AAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISKAT--
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APPLICATION NUMBER: US 07/704,289
FILING DATE: 22-MAY-1991
ATTORNEY/AGENI INFORMATION:
NAME: Relier, Stephen E.
REGISTRATION NUMBER: 31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08379259
Patent No. 5695939
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TYPE: amino acid
STRANDEDNESS: unknown;
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-379-259-9
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CLASSIFICATION: 435
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STATE: California
COUNTRY: United St
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Best Local Similarity
Matches 132; Conserv
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192 AADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQ 251
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                         123 AAFLGQISHETIGGWATAPDGPYAWGYCFVRERNPSICSATPQFPCAPGQQYYGRGPIQI 182
                                                             132 TGRSNYDLAGRALGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPT 191
                                                                                   84 AAFFGQISHETIGGIRGAAD-QFQWGYCFKEEISKAI--
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Job time: 745 sec
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C; Species: Hordeum vulgare (barley)
C; Species: Hordeum vulgare (barley)
C; Species: 10-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C; Accession: S48847
R; Bryngelsson, T.; Collinge, D.B.; Green, B.; Gummesson, P.O.; Kragh, K.; Thordal-Chr submitted to the EMBL Data Library, March 1994
A; Description: Purification, characterization and cDNA sequence of a basic chitinase A; Reference number: S48847
A; Accession: S48847
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A; Residues: 1-256 < RRY>
A; Cross-references: EMBL:X78671; NID:q563486; PIDN:CAA55344.1; PID:q563487
C; Genetics:
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C; Superfamily: plant chitinase; plant chitinase homology
C; Superda: glycosidase; hydrolase; polysaccharide degradation
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-256/Product: chitinase cht2a #status predicted <MAT>
F;31-255/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.9%; Score 1334; DB 2; Length 2 Best Local Similarity 98.4%; Pred. No. 2e-108; Matches 252; Conservative 1; Mismatches 3; Indels
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                                        T10802
S14948
T09687
JQ0965
T10810
S05426
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$20981
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Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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Title: Perfect score:

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Run on: MO

Scoring table:

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Maximum Minimum

RESULT 2 848848 chithase (EC 3.2.1.14) cht2b precursor - barley C;Species: Hordeum vulgare (barley)

241 241

δ qq

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Wildernate names: acidic chitinase PR-Q
C;Species: Nicotiana tabacum (common tobacco)
C;Species: Nicotiana tabacum (common tobacco)
C;Accession: S20738
R;Linthorst, H.J.M.; van Loon, L.C.; van Rossum, C.J.; Bol, J.F.; van Roekel
submitted to the RML Data Library, January 1990
A;Description: Constitutive expression of acidic and basic Chitinase in tran
A;Reference number: S20737
                                                                                 RRWIPTAADTAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYYIRYCGMLGTAIGGN 245
                            RGPIQLTGRSNYDLAGRAIGKDLYSNPDLYSTRAWFWTAQGNKPSCHNVAL 185
                                           SFPGFGTTGDDTARRKEIAAFFGQTSHETTGGSL-SAEPFTGGYCFVRQNDQ--SDRYYG 121
                                                                                                                                                                                                                                                 common tobacco
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ses 159; Conserv
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R;Payne, G.; Ahl, P.; Moyer, M.; Harper, A.; Beck, J.; Meins Jr., F.; Ryals, Proc. Natl. Acad. Sci. U.S.A. 87, 98-102, 1990
A;Title: Isolation of complementary DNA clones encoding pathogenesis-related A;Reference number: A34801; MUID:90115914
A;Accession: B34801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogenesis-related protein Q precursor - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKAISPPYYG 125
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          #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                                                                                                                                                                                                                                                                                                             IAAANTEPGEGTTGSADDIKRDLAAFEGGTSHETTGGTRGAADQFQWGYCFKEEISKATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALFCCVFFLFTT----GSLAQGIGSIVTSDLFNEMLKNRNDGRCPANGFYTYDAFIAAAN
                                                                                                                                                                                                                                                                                                                                      MARFAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAF
                                                                                                                                                                                                                                                                                                                                                                                                               1 MARYAAL----AALLLAVAVGGAAAQGYGSVITQSVYASMLPNRDNSQCPARGFYTYDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HNVALRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                              4;
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Pred. No. 7.7e-67;
                                                                                                                                                                                                                                                                                  252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50;
                                                                                                                                                                                                                                                                                  Score 1266; DB 2;
Pred. No. 1.6e-102;
); Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
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64.3%;
                                                                                                                                                                                                                                                                                  93.0%;
illarity 93.0%;
Conservative 9
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Best Local Similarity
Matches 160; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-253 <PAY>
                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 238; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                        Query Match
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Meu

C.J.; Bol, J.F.; van Roekel, J.;

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os/owa
chitines (EC 3.2.1.14) chil7 precursor - tomato
c;Species: Lycopersicon esculentum (tomato)
c;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S37342; S38837; S25635
R;Danhash, N; Magemakers, C.A.M; van Kan, J.A.L.; de Wit, P.J.G.M.
Plant Wol. Biol. 22, 1017-1029, 1993
A;Ritle: Molecular characterization of four chitinase cDNAs obtained from Cladosporiu
A;Recreace number: S37341; MUID:94003061
A;Accession: S37342
A;Molecule type: MRNA
A;Residues: 1-247 <DAN>
in transgenic to
                                                                                                                                                                                                                                                                                                                      ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVAL 185
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                                                                                                                           PID:919773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253;
                                                          A.Accession: $20738
A.Molecule type: mRNA
A.Residues: 1-253 CLIN>
A.Cross-references: EMBL:X51425; NID:919772; PIDN:CAA35789.1; F.
C.Superfamily: plant chittinase homology
C.Keywords: 91ycosidase; hydrolase; polysaccharide degradation
F)30-251/Pommin: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                     62.4%; Score 850.5; DB 2;
llarity 63.9%; Pred. No. 1.7e-66;
Conservative 33; Mismatches 50;
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Citinase (EC 3.2.1.14) PR-P - common tobacco
NyAlternate names: acidic chitinase PR-P
C; Species: Nicotiana tabacum (common tobacco)
C; Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C; Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C; Caccession: S20737
C; Accession: S20737
A; Description: Constitutive expression of acidic and basic Chitinase in transgenic to A; Reference number: S20737
A; Accession: S20737
A; Accession: S20737
A; Accession: S20737
A; Cross-references: EMRE: X51426; NID:q19770; PIDN:CAA35790.1; PID:q19771
C; Superfamily: plant chitinase; plant chitinase homology
C; Keywords: q1ycosidase; hydrolase; polysaccharide degradation
F;30-251/Domain: plant chitinase homology RPCH>
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N.Alternate names: endochitinase partI
C; Species: Lycopersicon chilense
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 22-Jun-1999
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 22-Jun-1999
C;Accession: S51588
R;Chan, R.D.; Yu, L.X.; Greer, A.F.; Cheriti, H.; Tabaeizadeh, Z.
Mol. Gen. Genet. 245, 195-202, 1994
A;Title: Isolation of an osmotic stress- and abscisic acid-induced gene encoding & A;Reference number: S51588; MuID:95115667
A;Reference number: S51588; MuID:95115667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 FPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YYGRGPIQLTGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                  LAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LECCVFFLFLT----GSLAQGIGSIVTNDLFNEMLKNRNDGRCPANGFYTYDAFIAAANS
                                                                                                       HNVALRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRXCGMLGT
                                                                                                                                    7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.0%; Score 817.5; DB 2;
61.4%; Pred. No. 1.2e-63;
iive 34; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153; Conservative
                                                                                                                                                                                                                    241 ATGGNLDCYTQRNFA 255
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Best Local Similarity
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A; Residues: 1-250 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 DCYTQRNFA 255
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                     123
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N.Alternate names: endochitimase pcht28
C;Species: Lycopersicon chilense
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C;Accession: S51589
R;Chen, R.D.; Yu, L.X.; Greer, A.F.; Cheriti, H.; Tabaeizadeh, Z.
Mol. Gen. Genet. 245, 195-202, 1994
A;Title: Isolation of an osmotic stress- and abscisic acid-induced gene encoding an acid A;Reference number: S51588; MUID:95115667
A;Accession: S51589
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A; Resigues: 1-253 < CHE>
A; Cross-references: EMBL:119342; NID:g437018; PIDN:AAA64999.1; PID:g767828
C; Genetics:
C; Genetics:
C; Superfamily: plant chitinase; plant chitinase homology
C; Keywords: glycosidase; hydrolase
F; 1-24/Domain: signal sequence #status predicted <SIG>F; 1-24/Domain: signal sequence #status predicted <MAT>
F; 30-251/Domain: plant chitinase #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 AANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 GPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RWIPTAADIAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGIAIGGNL 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 FPGFGTTGDDTARKKEIAAFFCQTSHETTGGSLSADGPFAGGYCFVREGNOMGS-GFYGR 116
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A; Cross-references: EMBL: 215139; NID: 919186; PIDN: CAA78844.1; PID: 919187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 253;
                                                                                                                                                                                                                                                                                                                                 Length 247;
                                                     A; Molecule type: protein
A; Residues: 112-115;183-188;218-221 CDG0=0: 112-115;183-188;218-221 CJG0=0: 112-115;183-188;218-221 CJG0=0: CJG1/T
C; Superfamily: plant chitinase; plant chitinase homology
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
F; 17-16/Domain: signal sequence #status predicted <SIG>F; 17-24//Product: chitinase chil; #status predicted <MAT>F; 22-245/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.8%; Score 828.5; DB 2; 61.6%; Pred. No. 1.4e-64;
                                                                                                                                                                                                                                                                                                                              Query Match
62.4%; Score 850; DB 2;
Best Local Similarity 63.5%; Pred. No. 1.8e-66;
Matches 158; Conservative 34; Mismatches 53
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Best Local Similarity 61.69
Matches 157; Conservative
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pathogenesis-related protein P precursor - common tobacco C.Species: Nicotiana tabacum (common tobacco) C.Species: Nicotiana tabacum (common tobacco) C.Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 22-Jun-1999 C.Accession: A34801 B.P. Moyer, M.; Harper, A.; Beck, J.; Meins Jr., F.; Ryals, J. Proc. Natl. Acad. Sci. U.S.A. 87, 98-102, 1990 A.Title: Isolation of complementary DNA clones encoding pathogenesis-related proteins A; Reference number: A34801, MUID:90115914
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R; Kim, C.Y.; Gal, S.W.; Choe, M.S.; Jeong, S.Y.; Lee, S.I.; Cheong, Y.H.; Lee, S.H.; Plant Mol. Biol. 37, 523-534, 1998
A; Title: A new class II rice chitinase, Rcht2, whose induction by fungal elicitor is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Reference number: 214820; MUID:99278381
A Accession: T03017
A Status: preliminary; translated from GB/EMBL/DDBJ
A Status: preliminary; translated from GB/EMBL/DDBJ
A Status: 1-175 < KIM>
A Residues: 1-175 < KIM>
A Cross-references: EMBL:140338; NID:92340042; PIDN:AAC37516.1; PID:92340043
A Estimental source: cv. Cheongcheongbyeo
C Function: catalyzes the hydrolysis of the beta-1,4-N-acetyl-D-glucosamin
C; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                           C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 DLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQLTGRSNYDLAG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 RAIGKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCHNVALRRWTPTAADTAAGRVP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LFCCVFFLFLT---GSLAQGIGSIVINDLFNEMLKNRNDGRCPANGFYTYDAFIAAANS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
185 WIPSAADISANRVPGYGVIINIINGGIECGKGQNARVEDRIGYYRRNVSIMNVAPGDNLD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:9170312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFAS 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                              probable chitinase (EC 3.2.1.14) class II - rice (fragment) N,Alternate names: class II acidic chitinase; Rcht2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.4%; Score 808.5; DB 2; 61.0%; Pred. No. 7.5e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 814; DB 2; 1
Pred. No. 1.7e-63;
3; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.8%; Score 814; DB ilarity 83.4%; Pred. No. 1.7e Conservative 13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 61.0%
watches 152, Conservative
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A; Residues: 1-253 <PAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                             252
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                                                                                                          248 CYTORNEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simil
Matches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chitinase (EC 3.2.1.14) - garden petunia
NiAlternate names: acidic chitinase
NiAlternate names: acidic chitinase
NiAlternate names: acidic chitinase
NiAlternate names: acidic chitinase
Cipecas: Petunia x hybrida (garden petunia)
Cipecas: Petunia x hybrida (garden petunia)
Cipecas: Petunia x hybrida (garden petunia)
Cipecas: Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
CiAccession: $20741
A: Rinthorst, H.J.M.; van Loon, L.C.; van Rossum, C.J.; Bol, J.F.; van Roekel, J.; Meulen submitted to the EMBL Data Library, January 1990
A: Reference number: $20737
A: Reference number: $20737
A: Reference number: $20741
A: Moleule type: mRNA
A: Residues: 1-254 <LINA
A: Res
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGFGTTGDDTARKKEIAAFFGQTSHETTGGTLSPDGPYAGGYCFLRE-GNQMGNGYYGRG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 TPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 GTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRW 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
         A;Cross-references: EMBL:M97210; NID:g310936; PIDN:AAA64998.1; PID:g767827
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                               11 AAALLLAVAAGGAAAQGVGSVITRSVXASMLPNRDNSLCPARGFYTYDAFIAAANTFPGF 70
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTF
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                                                                                                                                                                                                                                                                                                                        Length 250;
                                                                                                                                                                       <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                             A Gene: pchtl
C:Superfamily: plant chitinase; plant chitinase homology
C:Keywords: glycosidase; hydrolase
F:1-21/Domain: signal sequence (fragment) #status predicted
F:22-250/Product: chitinase #status predicted <MAT>
F:27-248/Domain: plant chitinase homology <PGH>
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                                                                                                                                                                                                                                                                                                                           Score 816.5; DB 2;
Pred, No. 1.5e-63;
30; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.8%; Score 814.5; DB 2
llarity 62.1%; Pred. No. 2.3e-63;
Conservative 31; Mismatches 62
                                                                                                                                                                                                                                                                                                                               59.9%;
62.3%;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Matches 154; Conserv
                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            154;
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Best Local S:
Matches 154
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Savetal Saveta
A;Title: Molecular characterization of four chitinase cDNAs obtained from Cladosporiu A;Reference number: S37341; MUID:94003061
A;Accession: S37343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 YYGRGPIQLTGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 AANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 AANSFPGFGTAGDDTARKKEIAAFFGQTSHEFNGGSAGT---FTGGYCFVKQIEQ--SDR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-253 <DAN>
A;Cross-references: EMBL:215141; NID:g19188; PIDN:CAA78846.1; PID:g19189
A;Accession: S38839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 AALVALAVLAAALATAARAEQCGAQAGGARCPNCLCCSRWGWCGTTSDFCGDGCQSQCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RFAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 253;
                                                                                                                                                                                                                                                                                                                 A; gene: chi3
C; Superfamily: plant chitinase; plant chitinase homology
C; Superfamily: glycosidase; hydrolase; polysaccharide degradation
F;1-24/Domain: signal sequence #status predicted <51G>
F;25-233/product: chitinase chi3 #status predicted <MAT>
F;30-251/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.0%; Score 803.5; DB 2; 59.2%; Pred. No. 2e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ARFAALAVCAAALLLA-----VAAGGA
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Best Local Similarity 59.24
Matches 151; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 PTGENLDCNNOKNFA 251
                                                                                                                                                                                                                         A, Molecule type: protein
A, Residues: 134-152;225-228
C, Genetics:
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Best Local Similarity
Matches 162; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chitinase (EC 3.2.1.14) class II - peanut
C) Species: Arachis hypogaea (peanut)
C) Species: Arachis hypogaea (peanut)
C) Species: Arachis hypogaea (peanut)
C) Accession: 565070
R; Kellmann, J.W.; Kleinow, T.; Engelhardt, K.; Philipp, C.; Wegener, D.; Schell, J.; Scheller Mol. Biol. 30, 351-358, 1996
A; Title: Characterization of two class II chitinase genes from peanut and expression stuby. A; Reference number: 565069; MUID: 96178874
A; Accession: 565070
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: DNA
A; Resideas: 1-264 < KEL>
A; Cross-references: EMBL: X82330; NID: 91237026; PIDN: CAA57774.1; PID: 91237027
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S37343
chithnase (EC 3.2.1.14) chi3 precursor - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Species: 11-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S37343; S38839; S25636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKATSPP----YYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWF 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AARAFPAFGTTG - DDVTRKRELAAFFGQTSHETTGGTTNAPDEFEWGYCFLREQTKEQH 119
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                                                                                                                                                186
                                                                                                                                                                                RWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNL 246
                                                                                                                                                                                                                                                                                                     183 SWIPSAADQSANRAPGCGVITNIINGGIECGVGPNAAVEDRIGYXRRYCGMLNVAPGDNL 242
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                               FPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGR
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Plant Mol. Biol. 22, 1017-1029, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 95/1; 143/2
C;Superfamily: plant chitinase; plant chitinase homology
C;Keywords: glycosidase; hydrolase
F;30-264/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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Best Local Similarity 57.4%; Pred. No. 1.4e-62;
Matches 152; Conservative 35; Mismatches 63
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RESULT 15
$39979
chitimase (EC 3.2.1.14) - rice
C;Species: Oryza sativa (rice)
C;Accession: S39979
R;Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.
MOI. Genet. 241, 1-10, 1993
A;Title: Sequence variation, differential expression and chromosomal location of rice cha;Reference number: S39979; MUID:94049667
A;Reference rumber: S39979; MUID:94049667
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-339 FMBL:X56787
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Superfamily: lectin-related plant chitinase; polysaccharide degradation
F;33-74/Domain: hevein chitinase homology <PCH>
F;91-329/Domain: plant chitinase homology <PCH>
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                                                                                                                                                                                                                               250 GNKPSSHDVITGRWAPSPADAAAGRAPGYGVITNIVNGGLEGGHGPDDRVANRIGFYQRY 309
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                                                                          190 WPCAPGRKYYGRGPIQLSFNFNYGPAGRAIGVDLLSNPDLVATDATVSFKTALWFWATPQ 249
74 CGPTPTPTPPSPSDGVGSIVPRDLFERLLLHRNDGACPARGFYTYEAFLAAAAFPAFGG 133
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                                           TGSADDIKRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISKATSPP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.4%; Score 795; DB 2; L. 50.8%; Pred. No. 1.5e-61; Live 28; Mismatches 58;
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                                                                                                                                                                                                                                                                                               CGMLGTATGGNLDCYTQRNFAS 256
                                                                                                                                                                                                                                                                                                                           CGAFGIGTGGNLDCYNQRPFNS 331
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Search completed: May 3, 2002, 18:32:10 Job time: 7473 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

May 3, 2002, 18:33:16; Search time 78.59 Seconds (without alignments) 119.432 Million cell updates/sec Run on:

US-09-534-229C-1 1362 1 MARFAALAVCAAALLIAVAA.....MIGTATGGNLDCYTQRNFAS 256 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

100059 seqs, 36664827 residues Searched: 100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	7514	0	₩.	P29021 petunia hyb	m	Q05539 Lycopersico	1 hordeum v	3 brassic	5 hordeum vu	1 arabido	5 oryza	3 vitis v	7 pisum	9 gossypi	9	2	6 theobroma	1 phaseolu	Ŋ	5 solanum	9 nicotiana	1 nicotian	₹	m	P08252 nicotiana t	5	P21226 pisum sativ	8	7 lycopers	sningod 6,	9	i populus	snindod i
o o o o	CHIQ_TOBAC		CHIA_LYCCI		CHIP_TOBAC	CHIA_LYCES	- 1	CHI2_BRANA	CHI1_HORVU	CHIT_ARATH	CHI2_ORYSA	CHIB_VITVI	CHIX_PEA	CHI1_GOSHI	CHI1_ORYSA	CHIT_PHAVU	CHI1_THECC		CHI2_GOSHI		- 1	CHI2_TOBAC	- 1	CHI1_SOLTU	CHI1_TOBAC		CHI2_PEA	CHIC_LYCES	- 1	CHI6_POPTR	- 1	ار	CHI8_POPTR
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ery	62.7	62.4	8.09	59.8	59.4	59.0	56.7	56.4	55.4	55.1	54.9	54.3	53.1	53.1	53.0	52.8	52.7	52.2	52.2	52.1	52.0	51.8	51.8	51.8	51.5	51.3	51.3	50.8	9		\sim	S	41.6
Score	854.5	850	828.5	814.5	808.5	803.5	772	768	754.5	751	4	739.5		723	d	718.5		711.5		709	708	705.5	705	705	701	669	669	692	670	9	644.5	614	566.5
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ALIGNMENTS

CHIQ_TOBAC CHIQ_TOBAC IDD CHIQ_ DT CC CHIQ_ DT CC CHIQ_ DT CHIQ_
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                  185
                                                                                                                                                                                                                                                                                                                                                                                   RRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGN 245
                                                                                                                                                                                                                                                                                                                                                                                                182 GRWTPSAADQAANRVPGYGVIINIINGGIECGIGRNDAVEDRIGYYRRYCGMLNVAPGEN 241
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                              6 ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Mol. Biol. 22:1017-1029(1993).

-!- FUNCTION: THIS ACIDIC CHITINASE FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNCAL PATHOGENS.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- INDUCTION: BY FUNGAL INTECTION.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Būkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO CHITINNSE CLASS IB WHICH IS SIMILAR TO CLASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITINBINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Danhash N., Wagemakers C.A.M., van Kan J.A.L., de Wit P.J.G.M.: "Molecular characterization of four chitinase cDNAs obtained from Cladosporium fulvum-infected tomato.";
                                                                                                                                                                                                                                                                                                                                                  9 ALFCCVFFLFLT----GSLAQGIGSIVTSDLFNEMLKNRNDGRCPANGFYTYDAFIAAAN
                                                                                                                                                                                                                                                                                                 SFPGFGTTGDDTARRKEIAAFFGQTSHETTGGSL-SAEPFTGGTCFVRQNDQ--SDRYYG
                                                                                                                                                                                                                                                                                                                                  RGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 112-115; 182-188 AND 218-221
                                                                                                                                                                            Length 253;
                                                                                                                                                                                                       Indels
                                                                                                               ACIDIC ENDOCHITINASE Q.
Y -> F (IN STRAIN SAMSUN).
ODED41DEA99CE196 CRC64;
                                                                           Pathogenesis-related protein; Hydrolase; Glycosidase;
Chitin degradation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
ACIDIC 27 KDA ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                               DB 1;
                                                                                                                                                                              62.7%; Score 854.5; DB 1
64.3%; Pred. No. 3.7e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 AA
                                                                                                                                                                                                       Mismatches
  HSSP; P23951; 2BAA.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00182; Glyco_hydro_19; 1.
Prodom; PD000674; Glyco_hydro_19; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV. MONEYMAKER;
MEDLINE=94003061; PubMed=8400122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                       32;
                                                                                                                 253 AK
54 Y
27632 MW;
                                                                                                                                                                                Query Match 62.77
Best Local Similarity 64.33
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                 25 2
54
253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 LDCYNORNF 250
                                                                                                                                                                                                                                                                                                                                                                                                                                       LDCYTQRNF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHIB_LYCES
Q05540;
                                                                                                                                              SEQUENCE
                                                                                                                               VARIANT
                                                                                                        SIGNAL
                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHIB_LYCES
                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                     126
                                                                                                                                                                                                                                                                                                                                                            122
                                                                                                                                                                                                                                                                                                                                                                                     186
                                                                                                                                                                                                                                                                                                                                                                                                                                       246
                                                                                                                                                                                                                                                                                                            65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 FPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 LAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 850; DB 1; Length 247;
Pred. No. 8.5e-64;
1; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         ACIDIC 27 KDA ENDOCHITINASE. C1163ED1D272A5E5 CRC64;
                                                                                                                                                                                    PIR; S37342; S37344.

HSSP, P23951; ZBAA.

InterPro: IPR000726; Glyco_hydro_19.

Prom: P00102; Glyco_hydro_19; 1.

ProDom: P000757; Glyco_hydro_19; 1.

PROSITE: PS00774; CHITINASE_19_1; 1.

PROSITE: PS00774; CHITINASE_19_1; 1.

PROGENES: related protein; Hydrolase; Glycosidase; Chitin degradation; Signal.

SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q40114; Q40113;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ACIDIC ENDOCHITINASE PCHI28 PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: EXTRACELLULAR. INDUCTION: BY OSMOTIC STRESS AND ABSCISIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.4%; Score ... 563.5%; Pred. No. 8.5e-
+ive 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lycopersicon chilense (Solanum chilense)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 AA; 26583 MW;
                                                                                                                                                                           EMBL; Z15139; CAA78844.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 62.4%
Best Local Similarity 63.5%
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| ||||||||||
DCYDQRNFA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 DCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4083;
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Nicotiana tabacum (Common tobacco)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTORNEA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYNORNEA 252
                                                                                                                                                                        HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 AANSFPGFGTTGDDTARKKEIAAFFGQTSHETKGGSAGT---FTGGYCFVRQIDQ--SDR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 YYGRGPIQLIGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 AANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 RFAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Petunia hybrida (Petunia).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Viridiplantae, endicotyledons, core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HNVALRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGT
SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TUCLASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITINBINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                              R MBL; M97210; AAA64998.1; -
R HSSP; P23951; ZBRA.
R HSSP; P23951; ZBRA.
R HSSP; P23951; ZBRA.
R InterPro; IPR000726; Glyco_hydro_19.
R Profolus; Clyco_hydro_19; 1.
R PROSITE; PS00773; CHITINASE_19_1; 1.
R PROSITE; PS00774; CHITINASE_19_2; 1.
R CHAIN 25 253 ACIDIC ENDOCHITINASE PCHT28.
T CONFLICT 94 94 K -> N (IN REF. 1; AAA64998).
T CONFLICT 170 171 QD -> HH (IN REF. 1; AAA64998).
SEQUENCE 253 AA; 27569 MW; D48C269D5A794E60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linthorst H.J.M., van Loon L.C., van Rossum C.M.A., Mayer A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermātophyta; Magnoliophyta; eudicotyledons; core eudi
Asteridae; euasterids I; Solanales; Solanaceae; Petunia
                                                                                                                                                                                                                                                                                                                                                                                                                                    60.8%; Score 828.5; DB 1; 61.6%; Pred. No. 5.4e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
ACIDIC ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92033079; PubMed=2131096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
                                                                                                                                                                                          EMBL; L19342; AAA64999.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 PTGENLDCNNOKNFA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4102;
                                                 HYDROLASES)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Sim.
Matches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHIT_PETHY
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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TID CHIT_P
AC P1012
DT 01-DEC
DT 01-DEC
DT 01-DEC
DT 02-DEC
DC ACIDIT
OC SPETITION
OC SPETITION
OC ASTERI
OX NCBL3
RN [1]
RP SEQUEN
RN FINDEN
RN MEDLIN
RN LIDTEN
RN LIDTEN
RN LIDTEN
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RN LIDTEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WIPSAADISANRVPGYGVITNIINGGIECGKGQNARVEDRIGYYRRNVSIMNVAPGDNLD 244
Bol J.E., van Roekel J., Meulenhof J., Conelissen B.J.C.;
"Analysis of acidic and basic chitinases from tobacco and petunia and
their constitutive expression in transgenic tobacco.";
Mol. Plant Microbe Interact. 3:252-258(1990).
-!- FUNCTION: THIS ACIDIC CHITINASE FUNCTIONS AS A DEFENSE AGAINST
-!- CATALYIC ACITATIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
-!- STRALT-D-GLIGOSAMINE POLYMERS OF CHITIN.
-!- STRALT-D-GLIGOSAMINE POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TO
CLASS IA IN THE CATALYIC PART BUT LACK A N-TERMINAL CHITIN-
BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127
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P17513;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
ACIDIC ENDOCHITINASE P PRECURSOR (EC 3.2.1.14) (PATHOGENESIS-RELATED PROTEIN P) (PR-P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AVCAAALLLAVAAGGAAAQGVGSVITRSVXASMLPNRDNSLCPARGFYTYDAFIAAANTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATESTATE STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT SVLALSEVVELETTGTLAQNVGSIVTSDLFDQMLKNRNDARCFAVRFYTYDAFTAAANSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.8%; Score 814.5; DB 1; Length 254; 62.1%; Pred. No. 7.8e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Draw, PRO00725, Glyco_hydro_19.

Prom. PF00182, Glyco_hydro_19.

Probom: PR000574; Glyco_hydro_19; 1.

PROSITE, PS00773; CHITINASE_19_1.

PROSITE, PS00774; CHITINASE_19_2; 1.

PRADAGENESIS-related protein; Hydrolase; Glycosidase; Chitin degradation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACIDIC ENDOCHITINASE.
377F494721B1E29B CF
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27665 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X51427; CAA35791.1; --
EMBL; A16118; CAA01262.1; --
PIR; S20741; S20741.
HSSP; P23951; ZBAA.
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                                                                                                                                Danhash N., Wagemakers C.A.M., van Kan J.A.L., de Wit P.J.G.M.;
"Molecular characterization of four chitinase cDNAs obtained from Cladosporium filtvum-infected formato.",
Plant Mol. Biol. 22:1017-1029(1993).
-!- FUNCTION: THIS ACIDIC CHITINASE FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNCAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon esculentum (Tomato).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
                                                                                           RWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- INDUCTION: BY FUNGAL INFECTION.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TCCIASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.0%; score 803.5; DB 1; Length 253; 59.2%; Pred. No. 6.4e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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ACIDIC 26 KDA ENDOCHITINASE.
6C78CA3750DE6D7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1)
SEQUENCE FROM N.A., AND SEQUENCE OF 134-152 AND 225-228
SEQUENCE OF MONEYMAKER;
MEDLINE=94003061; PubMed=8400122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Promi Prof. 12. Clyco-hydro_19; 1. Prodom; Pro0182; Clyco-hydro_19; 1. Prodom; Pro00574; CHTINASE_19_1: 1. PROSITE; PS00774; CHTINASE_19_1: 1. Prof. 15. Prof. 2. CHTINASE_19_1: 1. Prof. 2. Chtil Charles Cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
ACIDIC 26 KDA ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                              253 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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01-JUN-1994 (Rel. 29,
01-OCT-1994 (Rel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHIA_LYCES
Q05539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
CHIA_LYCES
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                                                                                                         187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERAIN=CV. SAMSUN: IISSUD=Leaf;
MEDLINE-2033079; PubMed=21311096;
Linthorst H.J.M., van Loon L.C., van Rossum C.M.A., Mayer A.,
Linthorst H.J.M., van Loon L.C., van Rossum C.M.A., Mayer A.,
Landlysis of acidic and basic chitinases from tobacco and petunia and
their constitutive expression in transgenic tobacco.";
MAND. Plant Microbe Interact. 3:252-258(1990).
-i- FUNCTION: THIS ACIDIC CHITINASE FUNCTIONS AS A DEFENSE AGAINST
                                                                                                                                                                                                                                                                                                                       "Isolation of complementary DNA clones encoding pathogenesis-related proteins P and Q, two acidic chitinases from tobacco."; Proc. Natl. Acad. Sci. U.S.A. 87:98-102(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHITIN CONTAINING FUNGAL PATHOGENS.
-:- CATALYTIC ACTIVITY: HYDROLYGIS OF THE 1,4-BETA-LINKAGES OF
--- N-ACETYL-D-GLOCOSAMINE POLYMERS OF CHITIN.
--- SUBCELLULAR LOCATION: EXTRACELLULAR FLUID FROM LEAVES.
-:- INDUCTION: DURING LOCAL NECROTIC RESPONSE TO THE TOBACCO MOSAIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFCCVFFLFLT----GSLAQGIGSIVTNDLFNEMLKNRNDGRCPANGFYTYDAFIAAANS
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                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TUCLASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITINBINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 253;
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EMBL, X5146; CAA35790.1; -.
PIR, A34601; A24801.
PIR, S20737; S20737.
INTERPORT PR000726; Glyco_hydro_19.
From: PF00182; Glyco_hydro_19; I.
Propon: PP000574; Glyco_hydro_19; I.
PROSITE; PS00773; CHITINASE_19_1; I.
PROSITE; PS00774; CHITINASE_19_2; I.
PRACHORESIS-related protein; Hydrolase; Glycosidase; Chitich Advanced Astron.
                                                                                                                                                                                                                                     Payne G., Ahl P., Moyer M., Harper A., Beck J., Meins F. Ryals J.;
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C -> Y (IN STRAIN SAMSUN).
AA49930C0A0C3E50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.4%; Score 808.5; DB 1;
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                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL S
STRAIN-CV. XANTHI NC;
MEDLINE-90115914; PubMed-2296608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27469 MW;
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SIGNAL 1 24
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Best Local Similarity
Matches 152; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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EMBL; L34210; AAA56786.1;
EMBL; M62904; AAA32941.1;
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                                                                                                                                                        122
                                                                                          YYGRGPIQLTGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                                                                                                                                                                                                                                                                                 01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
26 KDA ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14) (CHI-26).
Hordeum vulgare (Barley).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
                 61
                                                        -; - FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
-; - CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
     AANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
SIMILARITY: BELONGS TO CHITINASE CLEASS IB WHICH IS SIMILAR TC
CLASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITIN-
BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                           HNVALRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-93132784; PubMed-8421299;
Hart P.J., Monzingo A.F., Ready M.P., Ernst S.R., Robertus J.D.;
"Crystal structure of an endochitinase from Hordeum vulgare L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leah R., Tommerup H., Svendsen I., Mundy J.;
Bjochemical and molecular characterization of three barley seed
"Bjochemical and molecular characterization of three barley seed
proteins with antifungal properties.";
J. Biol. Chem. 266:1564-1573(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leah R., Mikkelsen J.D., Mundy J., Svendsen I.; "Identification of a 28,000 dalton endochitinase in barley
                                                                                                                                                                                                                                                                                  266 AA
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PRELIMINARY SEQUENCE OF 24-77 AND 148-188.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carlsberg Res. Commun. 52:31-37(1987).
                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. PIGGY;
MEDLINE=91107649; PubMed=1899089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biol. 229:189-193(1993).
                                                                                                                                                                                              ATGGNIDCYTQRNFA 255
                                                                                                                                                                                                             || || || || || || PTGENLDCNNQKNFA 251
                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4513;
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P23951;
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172 TAQGNKPSCHNVALRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYY 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLAVVVAVVATVAMAIGTARGSVSSIVSRAQFDRMLLHRNDGACQAKGFYTYDAFVAAAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ALAVCAAALLLAVAAAGGAAAQGYGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ATSPPYYGRGPIQLFGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWM
                                                          Glycosidase; Chitin degradation; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                            AA SEQUENCE)
AA SEQUENCE)
                                                                                                                                                                                                                                                                                                                                                                                                              Length 266;
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                                                                                                                                                                                                                                                                                                                                                                                         0949BE88CC20B664 CRC64;
                                                                          26 KDA ENDOCHITINASE
                                                                                                                                                                                                                                                                                                                                                                                                               56.7%; Score 772; DB 1;
56.8%; Pred. No. 2.8e-57;
cive 31; Mismatches 69;
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            PDB; 2BAA; 15-7AN-96.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00182; Glyco_hydro_19; 1.
Probom; PD000574; Glyco_hydro_19; 1.
PROSITE; PS00773; CHITINASE_19_1:
PROSITE; PS00774; CHITINASE_19_2; 1.
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PIR; A38664; A38664.
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634
747
744
99
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Best Local Simi
Matches 150;
                                                            Hydrolase;
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DISULFID
VARIANT
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DISULFID
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CHIL_HORVU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
FroDom; PD000609; c....
SWART; SW00270; ChtBD1; 1.
PROSITE; PS00026; CHITINARE.19_1: 1.
PROSITE; PS00774; CHITINARE.19_1: 1.
PROSITE; PS00774; CHITINARE_19_2; 1.
""Arolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-94143492; bubmed-8310072;
MEDLINE-94143492; bubmed-8310072;
Mucleotide sequence of a Brassica napus endochitinase gene.";
Plant Physiol. 101:1403-1403(1993).
-!- CARALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BFTA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SIMILARIY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CLASS IB IN THE CAPALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
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X SIMILARITY.
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E62EB4B17211DBCD CRC64;
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CHITIN-BINDING (BY S
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                          01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
10-0cT-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE CH25 PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                     322 AA.
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Interpro; IPR000002; Glyco_hydro_19.
Pfan; PF00187; Chitin_binding; 1.
Pfan; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
PPCDOM; PD0000544; Glyco_hydro_19; 1.
Probom; PD00005099; Chitin_bind; 1.
                                                                                                                                                                                                                                                                        PRT;
                                                                                                                    243 KRYCDILGVGYGNNLDCYSQRPFA 266
                                                                                232 TRYCGMLGTATGGNLDCYTQRNFA 255
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Best Local Similarity 58.4%
Matches 142; Conservative
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica napus (Rape)
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322 AA;
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CHIZ BRANA
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5

14; Gaps

55; Indels

Mismatches

32;

28 VGSVIIRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTIGSADDIKRDLAAFF 87

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                                                                                                                                                    34 RSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCHNVALRRWTPTAA 193
71 LSGIISRSQFDDMLKHRNDNACPARGFYTYDAFINAAKSFPGFGTTGDTATRKKEIAAFF 130
                                        88 GQTSHETTGGTRGAAD-QFQWGYCFKEEISK------ATSPPYYGRGPIQLTG 133
                                                                    Hordeum vilgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - :- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
- :- CATALATIC ACTUTY: HIDDLESS OF THE 1,4 BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
- :- INDUCTION: BY ETHYLENE.
- :- INDUCTION: BY ETHYLENE.
- :- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                              DTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEGUENCE FROM N.A. STRAIN-GV. NK 15SP TISSUE-Leaf; STRAIN-GV. NK 15SP TISSUE-Leaf; Ignatius S.W. 15P4), withukrishnan S.; Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1989 (Rel. 12, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
26 KDA ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 AA.
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EMBL; X15349; CAA33407.1; -.
PIR; S04131; S04131.
HSSP; P23951; 2BAA.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRIMTS; PR00451; CHITINBINDNG.
PRODOM; P000054; Glyco_hydro_19; 1.
ProDom; P000054; Glyco_hydro_19; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 PSSHAVITGQWSPSGTDRAAGRVPGFGVITNIVNGGIECGHGQDSRVADRIGFYRRYCDI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 PSCHNVALRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGM 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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SMART; SM00270; ChtBD1; 1.
SMOSITE: PS00773; CHITINASE_19_1; 1.
PROSITE: PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 ATSPPYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                              Length 318;
                                                                                                                                                      26 KDA ENDOCHITINASE 1.
CHITIN-BINDING (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   71; Indels
                                                                                                                                                                                                                                                             SIMILARITY.
SIMILARITY.
42D62B2FE8041954 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                           55.4%; Score 754.5; DB 1
48.1%; Pred. No. 9.5e-56;
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01-FPB-1991 (Rel. 17, Last sequence update)
01-FPB-1991 (Rel. 36, Last annotation update)
BASIC ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
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                                                                                                                                   POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        153; Conservative
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                                                                                                                                   318
62
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20
22
31
31
53
318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                       Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHIT_ARATH P19171;
                                                                                                                                                            CHAIN
DOMAIN
DISULFID
                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                   SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 RSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCHNVALRRWTPTAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 DRAAGRIPGYGVITNIINGGLECGRGQDGRVADRIGFYQRYCNIFGVNFGVNEGNLDCYNQRS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ATSPPYYGRGPIQLTG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 VGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLAAFF 87
                                 -- CAMALATIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GIDCOSAMINE POLYMERS OF CHITIN.
-- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
-- ITSSUE SPECIFICITY: HIGH CONSTITUTIVE LEVEL IN ROOTS WITH LOWER LEVELS IN LEAVES AND FLOWERSON.
-- INDUCTION: FRHYLENE INDUCES HIGH LEVELS OF SYSTEMIC EXPRESSION OF BASIC CHITINASE WITH EXPRESSION INCREASING WITH PLANT AGE.
-- SIMILARIY: BELONGS TO CHITINASE CLASS IN WHICH IS SIMILAR TO CLASS IB IN THE CAPALITY. PART BUT WHICH INCLUDE A N-TERMINAL CHARIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chitin degradation; Chitin-binding; Signal
Res. 7:217-221(2000).
FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REMOVED IN MATURE FORM (PROBABLE) CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.1%; Score 751; DB 1; Length 322; 56.8%; Pred. No. 1.9e-55; Live 35; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY.
SIMILARITY.
C9AFFE4C544FCCD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASIC ENDOCHITINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQTSHETTGGTRGAAD-QFQWGYCFKEEISK---"--
                                                                                                                                                                                                                                                                                                                                          EMBL, M38240; ARA32769.1; ALL_INIT.
EMBL; AP002047; BAB03157.1; -
HSSP; P23951, 2BAA.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR00726; Glyco_hydro_19.
Pfam; PF00182; chitin_binding; 1.
Pfam; PF00182; Chitin_binding; 1.
Propon; PP000451; CHITINBINDIG.
Propon; PD000574; Glyco_hydro_19; 1.
PROSITE; PS000274; CHITIN_BINDIG; 1.
PROSITE; PS00026; CHITIN_BINDIG; 1.
PROSITE; PS00073; CHITIN_BINDIG; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
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315
522
63
83
84
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81
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83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
316
21
23
32
37
56
322 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
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Best Local S
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PROPEP
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Matches
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FVN 315

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250 TGQWTPSADDQRAGRVPGYGVITNIINGGLECGHGEDDRIADRIGFYKRYCDILGVSYGA 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multigene family.
SIGNAL 1
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                              NCBI_TaxID=29760;
                            245 NLDCYTOR 252
                                                310 NLDCYSQR 317
                                                                                                                                                                                                                                                                                                                                                                                                             HYDROLASES).
                                                                                                         CHIB_VITVI
                                                                                                                                                                                                                                                                                                                        challenge.
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Best Local
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                                                                                                                   P51613;
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                                                                                             CHIB_VITVI
                                                                                                          δy
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;
                                                                                                                                                                                                                                                                                                                   HYDROLASES).

PIR; SISS97; S1997; BLOUNGS TO FAMILY 19 OF GLYCOSYL.

BR HSSP; P23951; 2BAA.

DR InterPro; PR001002; Chitin_bind.

DR InterPro; IPR001002; Chitin_bind.

DR Pfam; PF00187; chitin_binding.

Pfam; PF00187; chitin_binding.

DR PRINTS; PR00451; CHITINBIRDNG.

DR PRODOM; PD000609; Chitin_bind; 1.

DR SMART; SM00270; Chitin_bind; 1.

DR SMART; SM00270; CHILIN_BINDS; 1.

DR PROSITE; PS00026; CHITIN_BINDS; 1.

DR PROSITE; PS00026; CHITIN_BINDS; 1.

DR PROSITE; PS00773; CHITINASE_19_1; 1.

DR PROSITE; PS00774; CHITINASE_19_2; 1.

MULLigane family: 21 pormermer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 ASGGGGSGVASIVSRSLFDLMLLHRNDAACPASNFYTYDAFVAAASAFPGFAAAGDADTN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCHNVA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 LRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMEGTATGG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ATSPPYY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 AGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDI 79
                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CHITIN-BINNING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 KREVAAFLAQTSHETTGGWATAPDGPYTWGYCFKEENGGAGPDYCQQSAQWPCAAGKKYY
                                                                                                                   Aruio.
Orgza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                    chitinase.";
Mol. Genet. 226:289-296(1991).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhu Q., Lamb C.J.; \fill^{\prime} "Isolation and characterization of a rice gene encoding a basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
BASIC ENDOCHITINASE 2.
CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY.
SIMILARITY.
7F4EC126265DEA84 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.9%; Score 747.5; DB 1
57.3%; Pred. No. 3.8e-55;
ive 28; Mismatches 63
                                                              01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-DC-1992 (Rel. 24, Last annotation update)
BASIC ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 AA
                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=91238706; PubMed=2034221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ММ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3336
3336
339
452
522
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 142; Conser
                                                                                                                                                                   NCBI_TaxID=4530;
                                           CHI2_ORYSA
P25765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DISULFID
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                              RESULT
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                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; Vitaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR00102; Chitin_bind.
InterPro; IPR00102; Chitin_bind.
InterPro; IPR00102; Clitin_binding.
Pfam; PF00187; chitin_binding; 1.
Prim; PF00182; Glyco_hydro_19; 1.
Prim; PF000574; Glyco_hydro_19; 1.
ProDom; PD00059; Chitin_bind; 1.
SWART; SW00270; Chitin_bind; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Physiol. 115:1029-1038(1997).

-1. FUNCTION: DEPENDER AGAINAST CHITIN CONTAINING FUNGAL PATHOGENS.

-1. CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4 BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

-1. SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHATIN BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Busam G., Kassemeyer H.H., Matern U.; "Differential expression of chitinases in Vitis vinifera L. responding to systemic acquired resistance activators or fungal challenge."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
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Y SIMILARITY.
Y SIMILARITY.
S SIMILARITY.
3802484ED69EC6C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASIC ENDOCHITINASE.
CHITIN-BINDING (BY S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 739.5; DB 1.
Pred. No. 1.7e-54;
                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
BASIC ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
314 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. PINOT;
MEDLINE=98052138; PubMed=9390436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z54234; CAA90970.1; -.
HSSP; P23951; ZBAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.3%;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314
61
61
38
44
51
                                                                                                                                                                                                               Vitis vinifera (Grape)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 AA;
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SMART;
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 7
                                                                                                                                                                             189
                                                                                                                                                                                                       240
                                                                                                                                                                                                                                249
                                                                                          121 AAFLAQTSHETTGGWASAPDGPYAWGYCYLREQGSPGAYCVPSAQWPCAAGRKYYGRGPI 180
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- CATALYTIC SCITULTY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-:- INDUCTION: BY FUNGAL INFECTION.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collinge D.B.;
"Accumulation of defence-related transcripts and cloning of a chitinase mRNA from pea leaves (Pisum sativum L.) inoculated with Ascochyta pisi Lib.";
Plant Sci. 92:69-79(1993).
-! - FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Embryophyta; Tracheophyta;
                                                                                                                                                                             130 QLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWT
                                                                                                                                                                                            PTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCY
                                                1 MGLWALVAFCLLSLILVGSAEQCGGQAGGRVCPGGACCSKFGWCGNTADYCGSGCQSQCS
                                                                                                                            --ATSPPYYGRGPI
                                                                          ---GVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatophyta; Magnollophyta; eudloctyledons; core eudlocts; Reurosids I; Fabales; Fabaceae; Papillonoideae; Vicieae; Pisum.
  51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV. BIRTE; TISSUF=Leaf;
Vad K., de Neergaard E., Madriz-Ordenana K., Mikkelsen J.D.,
    Indels
  78;
                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                            MARFAALAVCAAALLLA~--------VAAGGAAAQ--
                                                                                                                                                                                                                                                                                                                                                                          320 AA
    Mismatches
                                                                                                                               84 AAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pisum sativum (Garden pea).
Eukaryota, Viridiplantae, Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONTAINING FUNGAL PATHOGENS.
    30;
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HSSP; P02877; 1HEV.
      Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    250 TORNFAS 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                              301 NORPEGS 307
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                                                                                                                                                                                                                                                                                                                                                                           CHIX_PEA
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15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last sequence update)
ENDOCHITINASE I PRECURSOR (EC 3.2.1.14).
Gossypium hirsutum (Upland cotton).
EUMARYDAR, Viridiplantae; Streptophyta; Embryophyta; Iracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; spermatophyta; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 RRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 GRWTPSAADSSAGRVPGYGYTININGGIECGHGQDNRVDDRVGFYRRYCQIFGVDPGGN 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 RGPIQLTGRSNYDLAGRALGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVAL 185
                                                                                                                                                                                                                                                                                                                                                                                                                          ---ATSPPYYG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 KKKELAAFLAQTSHETTGGWPTAPDGPYAWGYCFVSEQNTQEVYCSPKDWPCAPGKKYYG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 AAGGAAAQGYGSVIIRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTIGSADD 78
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                             Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal; Multigene family: BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                           SIMILARITY)
                                                                                                                                                                                                                                                                                                                                   53.1%; Score 723; DB 1; Length 320; 55.6%; Pred. No. 4e-53;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                 7EDEC8C1AECC3435 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 IKRDLAAFFGOTSHETTGGTRGAAD-QFQWGYCFKEEISK----
                                                                                                                                                                                                                                                                                                                                                                        62;
                                                                                                                                                                                             (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 AA.
                                                                                                                                                                           ENDOCHITINASE. CHITIN-BINDING
                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
                                                                 PROSITE; PS00026; CHITIN_BINDING; PROSITE; PS00773; CHITINASE_19_1; PROSITE; PS00774; CHITINASE_19_2;
                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                      MW.
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320
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52
34507 N
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                                                       SM00270; ChtBD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 LDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 LDCNNORSFA 320
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Best Local Similarity
Matches 139; Conserv
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Q39799;
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                                                                                                                                                                                                 DOMAIN
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AGGAAAQGVG---SVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSA 76
                                                                                                                                     InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00107; chitin_binding; 1.
Pram; PF00182; Glyco_hydro_19.
Pram; PF00182; Glyco_hydro_19.
Probom; PP000574; Glyco_hydro_19; 1.
Probom; PD000509; Chitin_bind; 1.
SMART; SM00270: ChtBD1; 1.
PROSITE; PS00026; CHITIN_BINING; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00773; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 ATRKREIAAFLAQTSHETTGGAGWAAPDGPYAWGYCYNREINPPSSYCASDPNYPCAPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 PYYGRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVALRRWIPTAADTAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYYTRYCGMLGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                  ENDOCHITINASE 1.
REMOVED IN MATURE FORM (BY SIMI
CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.1%; Score 723; DB 1; Length 324; 53.3%; Pred. No. 4e-53; ive 35; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W, 9923B123EF5C7E3E CRC64;
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01-MAR-1992 (Rel. 21, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
BASIC ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 AA
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                                                                                                                                                                                                                                                                                                                                       BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MM;
                                                                                                                                                                                                                                                                                                                                   22
317
324
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53
53
                                                                                                            EMBL; U60197; AAB67842.1;
HSSP; P02877; 1HEV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.3
Matches 136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 TGGNLDCYTQRNFAS 256
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 AA;
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P24626;
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1D CHIL_O
AC PLANK
DT 01-MAR
DT 01-MAR
DT 01-DEC
DE BASIC
OS OYZA
OC EUKATY
OC SPERMA
OC EHCHAR
OX NCBL_T
RP SEQUEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 AAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADD 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00270; ChtBbl; 1.

PROSITE; PS00026; CHITINASE_19_1; 1.

PROSITE; PS00774; CHITINASE_19_2; 1.

Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal; SiGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 YGRGPIQITYNYNG-RGAGIGSDLINNPDLVASDA-VSFKTAFWFWATPQSPKPSCHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 ALRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATG
                                                                                                                                                   N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                              "Nucleotide sequence of a rice genomic clone that encodes a class
STRAIN-CV. JAPONICA; TISSUE-Seedling;
MEDLINE-91370895; PubMed=1893114;
Huang J.K., Wen L., Swegle M., Tran H.C., Thin T.H., Naylor H.M.,
Muthukrishnan S., Reeck G.R.;
                                                                                               Plant Mol. Biol. 16:479-480(1991).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                            CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASIC ENDOCHITINASE 1
CHITIN-BINDING (BY SI
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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Pred. No. 5.2e-53;
1; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 IKRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK---
                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P02877; 1HEV.
InterPro: IPR001002; Chitin_bind.
InterPro: IPR0010026; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDRG.
ProDom; PD000074; Glyco_hydro_19; 1.
ProDom; PD0000574; Glyco_hydro_19; 1.
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56.2%;
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Matches 141; Conservative
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305 DNLDCYNQRPY 315
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                                                                                    endochitinase.
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Search completed: May 3, 2002, 18:48:31 Job time: 915 sec

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May 3, 2002, 18:32:16; Search time 157.87 Seconds (without alignments) 237.193 Million cell updates/sec
                                                                                                                                                               US-09-534-229C-1
1362
1 MARFAALAVCAAALLLAVAA......MLGTATGGNLDCYTQRNFAS 256
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                          473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_bacteria:*
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sp_human:*
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sp_phage:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description				oryza	٠.	pordeu	oryza	oryza sa	solanum t	solanum	solanum	solanı		_		_		secale	Q9sxjl arabis gemm
SUMMARIES	Q1	043764	29axr8	243765	Q9FWE9	080423	09LEH7	Q9FWE7	004271	043835	658560	043834	022568	024007	082552	042515	043294	042839	Q9FRV0	Q9SXJ1
	DB II	10	10	10	10	1.0	10	10	10	10	10	10	10	10	10	10	10	10	10	10
		256	252	252	261	261	249	296	289	236	251	252	240	175	253				266	
949	Query	97.9	93.8	93.0	83.7	.82.9	82.8	73.4	71.5	9.09	60.4	60.4	60.2	59.8	59.4	59.1	58.6	56.7	56.4	56.3
	Score	1334	1277	1266	1139.5	1128.5	1128	1000	973.5	825.5	822.5	822.5	819.5	814	808.5	805.5	797.5	772.5	768	767
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Q9M7G7 Q9FRV1 Q9FPM1 Q42994 Q9M7H7	042993 09M7F6 P93680 080404	0997/64 0997761 0997772 09977740	042292 09M7G0 09M7F7 09M7G2 09SXJ4 09SXJ4	U95836 Q9M7F4 Q9M7G9 Q9SXJ2
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764 763 760.5 758.5 758	757 757 757 757 756.5	756 755 754 753 753	752 752 752 751 751	751 750 749 749
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ALIGNMENTS

	0;
RESULT 1 043764 PRELIMINARY; PRT; 256 AA. 043764 AC 043764 DT 01-NOV-1996 (TrEMBLrel. 01, Created) DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update) DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update) DT 01-UTW-2001 (TREMBLrel. 17, Last annotation update) DT 01-UTW-2001 (TREMBLrel. 17, Last annotation update) DE CHITINARSE (EG. 3.2.1.14) (CHITODEXTRINASE) (1.4-BETA-POLY-N-DE CHITANSE (EG. 3.2.1.14) (CHITODEXTRINASE) (2.4-BETA-FOLY-N-DE CHITANSE (EG. 3.2.1.14) (CHITODEXTRINASE) CHIAO OR CHT2A. OC HOACHUN VILIAGARE (BARLEY). SURATYOTA: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; CC Triticaes; Hordeum. OX TRAIN-CAY. PALLAS; RN [1] RN SEQUENCE FROM N.A. Thordal-Christensen H.; RA THORDAL-CHISTENSEN H.; THORDAL-CHISTENSEN H.; TOBMITTED (MAR-1994) to the EMBL/GenBank/DDBJ databases. 1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACHIOLOSAMINE POLYMERS OF CHITIN. DR ACHITLA (MAR-1994) to the EMBL/GenBank/DDBJ databases. CC ACATALYTIC ACTIVITY: HYDROLYSIS OF CHITIN. EMBL; X78671; CAA55344.1; DR MEDIS (MAR-1994) to the PAREL (MAR-1994) to the PAR	Ouery Match 97.9%; Score 1334; DB 10; Length 256; Best Local Similarity 98.4%; Pred. No. 6.3e-107; Matches 252; Conservative 1; Mismatches 3; Indels 0; Gaps OY IMARPALAVCAAALLLAVAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAF 60

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPYYGRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HNVALRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRXCGMLGT 240
                                                                                                             1 MARFAALAVCAAALLLAVAAGGAAAQGYGSVITRSVYASMLFNRDNSLCPARGFYTYDAF 60
                                                                                                 240
                              PPYYGRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                                                     SEQUENCE FROM N.A.
MEDLINE=2053799; Pubmed=11080301;
Yebh S., Moffatt B., Griffith M., Xiong F., Yang D.S.C., Wiseman S.B.
Sarhan F., Danyluk J., Xue Y.Q., Hew C.L., Doherty-Kirby A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
Triticeae; Secale.
NCBI_TaxID=4550;
                                                                                                                                                                                                                                                                                                                                                                                   in
                   IAAANTEPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATS
MARPAALAVCAAALLLAVAVGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAF
                                                                                                  HNVALRRWIPTAADIAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                             Lajoie G.; "Chitinase genes responsive to cold encode antifreeze proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 252;
                                                                                                                                                                                                                                        01-JUN-2001 (TIEMBLIEL 17, Last sequence update)
01-JUN-2001 (TIEMBLIEL 17, Last annotation update)
24.8 KDA CLASS II ENDOCHITINASE-ANTIFREEZE PROTEIN PRECURSOR Secale cereale (RYe).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              FC9D538F49690823 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 93.8%; Score 1277; DB 10; Best Local Similarity 93.8%; Pred. No. 4.9e-102; Matches 240; Conservative 7; Mismatches 5;
                                                                                                                                                                                                               252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                 winter cereals.";
Plant Physiol. 124:1251-1264(2000).
                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                26835 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF280438; AAG53610.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGNLDCYTQRNFAS 256
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                                                                                                                                                       241 ATGGNLDCYTQRNFAS 256
                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Q9AXR8
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RESULT

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240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 PPYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWEWMTAQGNKPSC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
                                                                                                                                    Hordeum vulgare (Barley).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.

NCBL_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Oryza sativa (Rice).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Sepernatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HNVALRRWIPTAADIAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MARFAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAF
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                                                                                                                                                                                                                                                                                                                                         OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252;
                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES
ACETYL-OGLOCOSAMINE POLYMERS OF CHITIN.
EMBL, X78672; CARA5345.1;
HSSP; P23951; 2BAA.
                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1.4-BEFA-POLY-N-ACETYLGLUCOSAMINIDASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAINS CLINE PO2; TISSUE-LEAF; STRAINS-CV. PALLAS, NEAR-ISOGENIC LINE PO2; TISSUE-LEAF; Bryngelsson T., Collinge D.B., Green B., Gummesson P.O., Thordal-Christensen H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8A6209D443E8FDD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1266; DB 10;
pred. No. 4.3e-101;
9; Mismatches 5;
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 AA.
252
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                                                                                                                                                                                                                                                                                                                                                                                                               Mendel, 25, Horru;Chiao;25.
Interpro; IPR000726; Glyco.hydro_19.
Priam; PR00182; Glyco.hydro_19; 1.
Probom; Pp000574; Glyco.hydro_19; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26629 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.08;
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Matches 238; Conservative
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   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 AA;
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01-JUN-2001 (
CHITINASE.
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     043765
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1;

Pred. No. 2.9e-89;

RP RA RA RA RA RI BR DR DR SQ

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9LEH7;
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                        Matches
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  SEQUENCE FROM N.A.

STRAIN-CV. NIPPONBARE;
Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
A Biaco J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
A Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
A Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
Andrenbush J., White O., Salzberg S.L., Fraser C.M.;
Constant C.L., Craven B. Otterback T.R., Khalak H., Feldblyum T.V.,
A Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

L. EMBL, ACG1633, AAG13608.1, d.

Bran, PF00182; Glyco_hydro_19; 1.

Probm; PD000574; Glyco_hydro_19; 1.

PROSITE; PS000773; CHITINASE_191; 1.

REQUENCE 261 AA, 27551 MW; 773133E7813DFDBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYYGRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVALRRWIPIAADIAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYYIRYCGMLGTA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 AANTFPGFGTT-GSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Titch Y., Yamamoto K., Sasaki T.;

"Nuclectide sequence of rice acidic class II chiitinase OsChiaZa.";

"Nuclectide sequence of rice acidic class II chiitinase OsChiaZa.";

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

HSPP, P2351; BAA31971; --

HSSP; P2351; 2BAA.

Mendel: 31086, Orysa; ChiaO; 31086.

InterPro; IPRO00726; Glyco_hydro_19.

Promom: PPO0182; Glyco_hydro_19; 1.

PROSITE; PSO0773; CHITINASE_19_1; 1.

PROSITE; PSO0774; CHITINASE_19_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
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Oryza satione.

Oryza satione.

Eukaryota; Viráiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                        83.7%; Score 1139.5; DB 10; Length 261; 82.7%; Pred. No. 3.2e-90; ive 20; Mismatches 23; Indels 1;
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Last annotation update)
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6760C2578121E0BF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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08,
17,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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01-NOV-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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Matches 211; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDAVVSFRTAMWEMMTAQGNKPSCHNVALREWTPTAADTAAGRVPGYGVITNIINGGLEC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                             122 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCH 181
                                                                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                             99
                          Gaps
                                                       3 RFRALAVÇARALLLAVARGGARAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 YASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLAAFFGQTSHETTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Green R.M., Bevan M.; "Isolation of genes induced in barley during powdery mildew infection."; submitted (JUL-2000) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                           182 NVALRRWIPTAADIAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGIA
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                          24; Indels
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Last sequence update)
Last annotation update)
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93.6%; Pred. No. 3e-89;
Live 8; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thesis (1991), University of Cambridge, UK EMBL, AJ276226; CAB99486.1; InterPro; PREMO0726; Glyco_hydro_19. Probom; PRO0182; Glyco_hydro_19; Probom; PD000574; Glyco_hydro_19; 1. PROSITE; PS00773; CHITIRASE_19-1; 1. PROSITE; PS00773; CHITIRASE_19-2; 1. SEQUENCE 249 AA; 27127 MW; ED85AB6E9E61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΩK
                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
82.0%; Pic
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 82.8
Best Local Similarity 93.6
Matches 206; Conservative
                              Conservative
                                                                                                                                                                                                                                                                                                                                                           242 TGGNLDCYTQRNFAS 256
                                                                                                                                                                                                                                                                                                                                                                                      247 YGSNLDCYNQRNFAS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                        TISSUE=LEAF;
                                                                                                           SEQUENCE OF 32-289 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Solanum tuberosum (Potato)
                                                                                                                                                                                                                                                                                                    Best Local Similarity 74.43
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 GNLDCYTORN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 SNLDCYNORN 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                    SECUENCE FROM N.A.
                                                                                                                          STRAIN-CV. IR36;
                              NCBI_TaxID=4530;
                                                                 STRAIN=IR36;
                                                                                                                                                                                                                                                                                            Query Match
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RA BUELL C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,

RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,

RA Hsiao J., Zismann V., Pai G., Bowman C.L., Fujic C.Y., VanAken S.E.,

RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,

RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;

RT "Oryza sativa chromosome 10 BAC OSJNBb0015111 genomic sequence.";

RUBL; ACO51633; AAG135901.;

DR EMBL; ACO51633; AAG135901.;

DR FRAD.; PRO00182; Glyco_hydro_19.

PROSITE: PSO00774; Glyco_hydro_19;

PRODOM: PDO0015; Glyco_hydro_19;

PROSITE: PSO00773; CHITNASE_19_1;

ROUGENCE 296 AA; 32169 MW; ICOF8158E5CF119B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 VSNPDLVSTDAVVSFRTAMWFWWTAQGNKPSCHNVALRRWTPTAADTAAGRVPGYGVITN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RSNYDLAGRAIGKDL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RFAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 RFVQLAACAVAVLLAVAASGAAAQGVGSVITEAVFNSMLPNRDNSLCPARGFYTYDAFTA 69
          150 IDAVYSFRTAIWFWMIAQGNKPSSHDVALGRWTPTAADTAAGRVPGYGVITNIINGGLEC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 AANTEPGFGTT-GSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSP
                                                                                                                                                                                          Oryza sativa (Rice).
Warayota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 IINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFAS 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 IINGREECDVGQNDANVDRIGYYKRYCDMLGADPGSNLDCYNQRDFDS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.4%; Score 1000; DB 10;
ilarity 67.7%; Pred. No. 3.6e-78;
Conservative 22; Mismatches 33;
                                 217 GMGRNDANYDRIGYYTRYCGMLGTATGGNLDCYTQRNFAS 256
                                               210 GMGQNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFAS
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                                                                                                                    296 AA.
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08,
17,
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01-WAR-2001 (TrEMBLrel. 16,
01-JUN-2001 (TrEMBLrel. 17,
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Best Local Similarity
Matches 195; Conserv
                                                                                                                                                                                PUTATIVE CHITINASE
                                                                                                                                                                                                                                         NCBI_TaxID=4530;
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01-NOV-1998
01-JUN-2001
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01-JUN-2001
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65 NIFPGFGTIGSA-DDIKRDLAAFFGQTSHETIGGTRGAADQFQWGYCFKEEISKATSPPY 123
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 ALRRWIPTAADIAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGIAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 VCAA----ALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.5%; Score 973.5; DB 10; Length 289; 74.4%; Pred. No. 6.6e-76; ive 19; Mismatches 38; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Mol. Biol. 35:749-761(1997).
                                                                                                                                                                                                                       Landing Land (APR 1997) to the EMBL/GenBank/DDBJ databases.

Submitted (APR 1997) to the EMBL/GenBank/DDBJ databases.

REMEL, AF013580; AAB50170.1; ...

REMEL, AF001500; AAB502380.1; ...

REMEL, AP001500; ABB502380.1; ...

REMEL, AP001500; ABB502380.1; ...

REMEL, AF001500; ABB502380.1; ...

REMEL, AF001500; ABA502380.1; ...

REMEL, AF001500; AP0070.14790.

REMEL, AF00182; Glyco_hydro_19; 1.

REMEL, AF00182; Glyco_hydro_19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pucuter K., Stromberg A., Schmelzer E., Kombrink E.;
"Primary structure and expression of acidic (class II)
potato.":
Yun C.-H., Lee B.P., Yun K.J., Eun M.Y.; Submitted (AUG-1997) to the EMBL/GenBank/DDBU databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CLASS II CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE)
ACETYLELUCOSAMINIDASE) (FOLY-BETA-GLUCOSAMINIDASE) (CHIAO OR CHTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV DATURA; TISSUE-LEAF;
MEDLINE-98088002; Pubmed-9426596;
Buchter R., Stromberg A., Schmelzer E., Kombrink
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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3;

NÔN_TER SEQUENCE

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--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPTAADTAAGRVPG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 AFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQLTGRSNYDLAGRAI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 AQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLA 84
                                                                                                       145 --GKDLVSNPDLVSTDAVVSFRIAMWFWMIAQGNKPSCHNVALRRWIPTAADTAAGRVPG 202
                                                      01-NOV-1996 (TIEMBLEEL. 01, Last sequence update)
01-UNY-2001 (TIEMBLEEL. 17, Last annotation update)
CLASS II CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 AQNAGSIVTRELEEQMLSFRNDVCPGKGFYTYDAFIAAANSFPAFGTTGDDTARKKEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridin lantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; dagnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                          22 AQNAGSIVTRELFEQMLSFRNNDVCPGKGFYTYDAFIAAANSFPAFGTTGDDTARKKEMA
                                 85 AFFGQISHETIGGIRGAADQFQWGYCFKEEISKAISPPYYGRGPIQLIGRSNYDLAGRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Mol. Biol. 35:749-761(1997).
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
                                                                                                                                                                                                 203 YGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27491 NW; 2DC63CEB2C319B31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. DATURA; TISSUR=LEAF;
MEDLINE=98088002; PubMed=9426596;
Buchter R., Stromberg A., Schmelzer E., Kombrink E.
"Primary structure and expression of acidic (class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.4%; Score 822.5; DB 1
65.7%; Pred. No. 5.2e-63;
live 28; Mismatches 45
                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                            252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P23951; 2BAA.
Mendel; 14796; Soltu;Chia0;14796.
InterPro; IPR000726; Glyco_hydro_19.
Propom; P000182; Glyco_hydro_19; 1.
Propom; P0000574; Glyco_hydro_19; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                   043834;
01-NCV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U49969; AAB96341.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          CHIAO OR CHTA2.
Solanum tuberosum (Potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 65.7
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Glycosidase.
SEOUENCE 252 AA; 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
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                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                 Q43834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 AQGVGSVIIRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLA 84
                                                                                                                                                                                                                                                                                                                                                                                                              AFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQLTGRSNYDLAGRAI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                 --GKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCHNVALRRWTPTAADTAAGRVPG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Solanum tuberosum (Potato).

Bukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Esparautophyta: Magnoliophyta: eudicotyledons: core eudicots: Asteridae: eusterida I; Solanales: Solanaceae: Solanum.
                                                                                                                                                                                                                                                                                                                                      25 AQGVGSVIIRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLA
                                                                                                                                                                                                                                                                                                                                                           7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 YGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Primary structure of potato acidid (class II) chitinase.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF024537; AAB81962.1; -.
HSSP; P23951; 2BAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.4%; Score 822.5; DB 10; Length
65.7%; Pred. No. 5.1e-63;
.ive 28; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 AA; 27359 MW; B4C63CF915319BlA CRC64;
                                                                                                                                                                                                                216C86B55D8CC7FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TIEMBLEEL. 13, Created)
01-MAY-2000 (TIEMBLEEL. 13, Last sequence update)
01-JUN-2001 (TIEMBLEEL. 17, Last annotation update)
CLASS II CHITINASE (EC 3.2.1.14) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-CV. DATURA; TISSUE-ELICITOR-TREATED LEAVES; Kombrink E.;
                                                                                                                                                                                                                                                                                                          44;
                                                                                                                                                                                                                                                                   60.6%; Score 825.5; DB 1
65.7%; Pred. No. 2.6e-63;
cive 29; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 AA
                    CHITIN.
               EMBL; U49970; AAB96340.1; -. HSSP; P23951; 2BAA.
HSSP; P23951; 2BAA.
Mendel; 14797; Soltu.Chia0;14797.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00182; Glyco_hydro_19.
ProDom; P000574; Glyco_hydro_19.
PROSITE; PS00774; CHITINASE_19_1; I.
PROSITE; PS00774; CHITINASE_19_1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pfam; PF00182; Glyco_hydro_19; 1.
Probom; PD000574; Glyco_hydro_19; 1.
PROSITE; PS00773; CHTRINASE_19_1; 1.
PROSITE; PS00774; CHIRINASE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000725; Glyco_hydro_19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                    236 AA; 25723 MW;
                                                                                                                                                                                                                                                                          Query Match 60.6%,
Best Local Similarity 65.7%,
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Glycosidase,
NON_TER 1
                                                                                                                                                                              Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153;
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QQ QΥ QQ II) chitinase in

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Gaps

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SEQUENCE

RESULT 10
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AC 095849
AC 01-MAX
DT 01-MAX
DT 01-MAX
DT 01-MAX
DE CLASS
GS CHTA3
GS SOLAN
CC SPECT

Query Match

Best Local

Matches

δă

; 0

Gaps

9

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REGULE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-CV. HANBYUL; TISSUE-LEAF;
RA HWANG B.K., Hong J.K., Kim Y.J.;
RA HWANG B.K., Hong J.K., Kim Y.J.;
RT = coolding and characterization of a pathogen-induced gene rencoding a basic class II chitinase from Caps.cum annuum.";
RT = chooling a basic class II chitinase from Caps.cum annuum.";
RT = submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
DR = MSSP; PA3951; 2BAA.
DR = HSSP; PA3951; 2BAA.
DR = RESP: PA3951; Capan;Chia0;33139.
DR = Fam: PF00182; Glyco.hydro.19.
DR = Fram: PF00182; Glyco.hydro.19.
DR = ProDom; PD00574; Glyco.hydro.19.
DR = PROSITE; PS00774; CHITINASE.19.2; 1.
DR = PROSITE; PS00774; CHITINASE.19.2; 1.
DR = PROSITE; PS00774; CHITINASE.19.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 ANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPY 123
                                                                                                                                                                                                                                                                                                                                                      82 DLAAFFGQTSHETTGGTRGAADQFUWGYCFKEEISKATSPPYYGRGPIQLTGRSNYDLAG 141
                                                                                                                                                                                                                                                                                                                                       142 RAIGKDIVSNPDIVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPTAADTAAGRVP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 FAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 GYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNPAS 256
Length 253;
                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                        Length 175;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                175 AA; 18969 MW; 48933B1BAFCB1FCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                        ; Score 814; DB 10;
; Pred. No. 1.8e-62;
13; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.4%; Score 808.5; DB 1
59.4%; Pred. No. 8.3e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                                                                                                                            59.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08,
08,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 59.4 Matches 151; Conservative
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                        Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHITINASE CLASS II. CHIAO OR CACHIZ.
                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                              146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                           NON_TER
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082552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              082552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 AFFCQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGFIQLTGRSNYDLAGRAI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 AQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPTAADTAAGRVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kim C.Y., Gal S.W., Choe M.S., Jeong S.Y., Lee S.I., Cheong Y.H., Lee S.H., Choi Y.J., Han C.D., Kang K.Y., Cho M.J.;
                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 YGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240;
                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum. NCBI_raxID-4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                               Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AF024538; AAB81963.1; -. HSSP; P23951; 2AB81963.1; -. HSSP; P23951; Soltu.Chia0;27051. InterPro; JFR000726; Glyco_hydro_19. ProDom; P0000526; Glyco_hydro_19. ProDom; P0000574; Glyco_hydro_19; 1. PROSITE; PS000773; CHITINASE_19_1; 1. PROSITE; PS00774; CHITINASE_19_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           240 AA; 26258 MW; 0B41665702B11709 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE (EC 3.2.1.14) (FRAGMENT).
                                                                                 01-JUN-2001 (TIEMBLEEL. 05, Last sequence update) 01-JUN-2001 (TIEMBLEEL. 17, Last annotation update) CLASS II CHITINASE (EC 3.2.1.14) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.2%; Score 819.5; DB 10; 65.2%; Pred. No. 8.8e-63; wismatches 44;
                                                                                                                                                                                                                                                  STRAIN-CV. DATURA; TISSUE-ELICITOR-TREATED LEAVES;
Kombrink E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Æ
                                                 AA.
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                                                                              Created)
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                                                 PRT;
                                                                              (TremBLrel. 05,
                                                                                                                                                       Solanum tuberosum (Potato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Glycosidase.
NON_TER 1 1
SEQUENCE 240 AA; 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=LEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152;
                                                                              01-JAN-1998
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                                                    022568
                                                                   022568
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                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. NC 4;

MEDLINE=96178874; PubMed=8616259;

MEDLINE=96178874; PubMed=8616259;

Rellmann J.W., Kleinow T., Engelhardt K., Philipp C., Wegener D.,

Schell J., Schreier P.H.;

Characterization of two class II chitinase genes from peanut and

"Characterization of two class II chitinase genes from peanut and

"Characterization of two class II chitinase genes from peanut and

"Characterization of two class II chitinase genes from peanut and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arachis hypogaea (Peanut).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; Papilionoideae; Arachis.
NCBI_TaxID=3818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RFAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIA 62
                                                                                                                                                                                                                  NVALRRWIPTAADIAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTA 241
                                                                             124 YGRGPIQLTGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KFCNFTFTLALIVVLQALGASADDAGTIITQPLYNFFLKHLTDSRCBAHGFYTYNAFVT
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                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 805.5; DB 10; Length 264;
Pred. No. 1.6e-61;
5; Mismatches 63; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Glycosidase.
SEQUENCE 264 AA; 28924 MW; CCB13C590ADB5D8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 AA.
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Best Local Similarity 57.4%;
Matches 152; Conservative 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                        242 TGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
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Q42515;
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240 FYKRYCDILKIGYGSNLDCANQQHF
230 YYTRYCGMLGTATGGNLDCYTQRNF
   δy
                      QQ
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3, 2002, 18:46:59 Search completed: May Job time: 883 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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using sw model protein search, protein ĕ May 3, 2002, 18:30:29; Search time 117.39 Seconds (without alignments) 203.814 Million cell updates/sec Run on:

US-09-534-229C-2 1792 1 MSTLRARCATAVLAVVLAAA......YGNNLDCYNQLSFNVGLAAQ Title: Perfect score: Sequence:

323

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

74073290 residues 522463 seqs, Searched: 522463 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB s Maximum DB s

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_1101:* 1: /SIDS2/mandat

/SIDSZ/gogdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSZ/gogdata/geneseq/geneseqp/AA1981.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp/AA2001 DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	wheat chitinase pr	Wheat chitinase pr	Rye chitinase-like	Rye chitinase-like	RCH10 chitinase pr	Rice chitinase. O	Amino acid sequenc	Tobacco intracellu	Nicotiana sp. intr	Amino acid sequenc	Basic chitinase 48
YES				-	-	_	œ.	•		10	7	m	_
SUMMARIES		£ £	AAB11488	AAB11489	AAW98079	AAW98080	AAR29019	AAR67969	AAB6744	AAR1327	AAW31297	AAB07513	AAR15841
			22	22	20	20	13	16	22	12	18	21	12
		Length	323	319	318	298	336	336	336	324	324	324	329
	оf	Query Match Length DB	100.0	72.2	72.0	70.6	9.89	68.6	68.6	65.7	65.7	65.7	65.3
		Score	1792	1294.5	1290	1265	1230	1230	1230	1177.5	1177.5	1177.5	1170
		Result No.	 	7	3	4	Ŋ	9	7	80	თ	10	11

Chitinase, Cucurb	Amorican olm chiti		100	of a	U	Floral organ-speci	Banana ripening fr	C. ensiformis chit	A maize chitinase	Petunia extracellu	Petunia hybrida ex	Amino acid sequenc	O	Wheat chitinase pr	Sugar beet chitina	Rye chitinase-like	Rye chitinase-like	Wild tomato endoch	A maize chitinase	Wild tomato endoch	Ų,	Arabidopsis thalia	Arabidopsis thalia		Amino acid sequenc	н.	acid	Sugar beet chitina	A maize chitinase	Sugar beet chitina	tdol	A maize chitinase
50	AAKLI3US	AAWUULBD	AAR20022	AAR20000	AAR52577	AAW64776	AAY 05844	AAW90169	AAB18902	AAR13274	AAW31296	AAB07512	AAR76714	AAB11487	AAR28150	AAW98081	AAW98082	AAR76713	AAB18903	AAR76712	AAB18905	AAG28415	AAG28414	AAB28788	AAB18906	AAB18904 ·	AAB18936	AAR28147		AAR28145	365	AAB18899
18	7 :	7 ;	7 L) (r	7 1	19	20	20	21	12	18	21	16	22	13	20	20	16	21	16	21	21	21	22	21	21	21	13	21	13	21	21
292	331	317	270	202	266	328	2466	24	259	254	254	254	253	256	439	252	230	250	252	253	284	272	280	372	155	271	271	268	281	264	813	328
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1163.5	1161	1160	1142.5	1141.5	1055	1052.5	930	879	827	818.5	818.5	818.5	809	798	795	790	786	779.5	779.5	775.5	774	770.5	770.5	707.5	644.5	633	633	97	595.5	584	492	480.5
12	13	14	م <u>ر</u>	9 F	- a	19	20	21	22	23	24	25	26	27	28	29	30	31	32	m	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAB11488 standard; protein; 323 AA. (first entry) 02-MAR-2001 AAB11488; AAB11488 RESULT

Wheat chitinase protein homologous to rye chitinase.

Wheat; chitinase; low temperature expression; hardened; plant; snow mould resistance; psychophilic plant pathogen; rye.

Triticum aestivum

JP2000270866-A.

03-OCT-2000.

99JP-0081694 25-MAR-1999; 99JP-0081694 25-MAR-1999; (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.

WPI; 2001-027417/04.

New low temperature expression chitinase gene for producing a plant grade highly resistant to psychophilic plant pathogenic microbes $\,$

Claim 4; Fig 2; 11pp; Japanese.

This invention describes novel wheat chitinase genes. The invention also describes a method for the isolation of a low temperature expression

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel wheat chitinase genes. The invention also describes a method for the isolation of a low temperature expression chitinase gene in which the mRNA is extracted from a fully hardened autumn wheat PII73438 (of high snow mould resistance). The genes are
chitinase gene in which the mRNA is extracted from a fully hardened autumn wheat PII73438 (of high snow mould resistance). The genes are useful for creating a plant grade, highly resistant to psychophilic plant pathogenic microbes.
                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                    SCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIF 300
                                                                                                                                                             61 RCQSQCTGCGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGT 120
                                                                                                                                                                                                    TGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCA 180
                                                                                                                                  Gaps
                                                                                                                       09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \boldsymbol{w} temperature expression chitinase gene for producing a plant highly resistant to psychophilic plant pathogenic microbes \cdot
                                                                                                                       1 MSTLRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP
                                                                                                                                                                                                                                           PGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wheat, chitinase; low temperature expression; hardened; plant; snow mould resistance; psychophilic plant pathogen; spring wheat.
                                                                                                    0;
                                                                                Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wheat chitinase protein homologous to spring wheat chitinase.
                                                                                                    Indels
                                                                               Query Match
100.0%; Score 1792; DB 22;
Best Local Similarity 100.0%; Pred. No. 2.6e-144;
Matches 323; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.
                                                                                                                                                                                                                                                                                                                                                                                               AAB11489 standard; protein; 319 AA
                                                                                                                                                                                                                                                                                                                                     301 GIGYGNNLDCYNQLSFNVGLAAQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Fig 3; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0081694
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum
                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP2000270866-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAB11489;
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                                                      Sequence
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AAB11489
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useful for creating a plant grade, highly resistant to psychophilic plant
pathogenic microbes.
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                                                                                                                                                                                                                                                                                                                                                       KQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                          72 G------GGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTIG 122
                                                                                                                                                                                                                                                                                                                 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHT9; chitinase-like protein; antifreeze protein; AFP; winter rye, antifungal; fungicide; cold tolerance; frost tolerance; transgenic plant; preservation; cryopreservation; tumour; therapy.
                                                                                                                                                                                       123 DIDTRKREVAAFFQQTSHETTGGWPTAPDGPFSWGXCFKQBQGSPPSYCDQSADWPCAPG
                                                                                                                                                                                                                                                                                                                                                                        12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "mature protein, also claimed in Claim 10"
                                                                                                     Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding antifreeze polypeptides from plants
                                                                                                                                     Indels
                                                                                                     DB 22;
                                                                                                                                     48;
                                                                                                  ; Score 1294.5; DB 22; Pred. No. 4.5e-102; 34; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rye chitinase-like protein CHT9 preprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW98079 standard; Protein; 318
                                                                                                         72.2%;
71.0%;
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                                                                                                     Query Match
Best Local Similarity 71.0%;
Matches 223; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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/note= "r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 GYGNNLDCYNQLSF 316
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305 sygdmldcyngrpf 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Griffith M, Hew C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-153795/13.
                                                            AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secale cereale.
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                                                            Sequence
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AAW98079
ID AAW98
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Secale cereale.

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The present sequence is winter rye (Secale cereal L. cv. Muskateer)
CHT9 preprotein. The mature protein, which is also claimed, is a
chitimese like protein that has chitimese (antifungal) and
antifreeze activities. CHT9 cDNA (see AAXX4889) was obtained by
isolating mRNA from rye plants grown at low temperatures in the
sheence of pathogens or other stresses, i.e. under conditions when
con protein and peast (First) have been cloned and expressed. CHT9
and CHT46 (see AAW98081-82) have been cloned and expressed in
confly chitimases with antifreeze activity would be expressed in
the chitimase-like antifreeze proteins can be used: to increase
freezing tolerance of plants and microorganisms; to increase field
survival of plants, animals and microorganisms exposed to sub-zero
temperatures; to inhibit ace recrystallisation in blological
materials or foods; for cryopreservation and hypothermic protection
of cells, embryos, tissues etc. (particularly human platelets); and
co kell; tumour cells. They are also used to inhibit initiation and
progression of diseases or spoilage caused by low temperature
cryopreserved biological meterial. The signal peptide can be used
cryopreserved biological meterial. The signal peptide can be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 tpvpvptptgggvssiisgslfdqmllhrndaaclakgfynygafiaaansfsgfattgg 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCH 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 dvitgrwspsgadqaagrvpgygvitniingglecgrgqdarvadrigfykrycdllgvs 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHT9; chitinase-like protein; antifreeze protein; AFP; winter rye; antifungal; fungicide; cold tolerance; frost tolerance; transgenic plant; preservation; cryopreservation; therapy.
particularly with chitinase activity, used to impart frost, and pathogen, resistant to plants, for preservation of foods, cells etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 LDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 vvvamlaaafavsahaeqcgsqaggatcpnclccskfgfcgstseycgdgcqsqcnrcgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1290; DB 20;
Pred. No. 1.1e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Mismatches
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                                                                                     Claim 10; Fig 21a; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.0%;
71.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223; Conservative
                                               for treating tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 ygdnidcyngrpf 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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The present sequence is winter rye (Secale cereal L. cv. Muskateer)

CHT9 mature protein. It lacks the 20-amino acid signal peptide

of the preprotein (see AAM98079), which is also claimed. Mature CHT9

is a chitinase-like protein that has chitinase (antifungal) and

antifreeze activities. CHT9 preprotein cDNA (see AAX24869) was

cobtained by isolating mRNA from rye plants grown at low temperatures

in the absence of pathogens or other stresses, i.e. under conditions

when only chitinases with antifreeze activity would be expressed.

CHT9 and CHT46 (see AAW98081-82) have been cloned and expressed.

CHT9 and CHT46 (see AAW98081-82) have been cloned and expressed in a bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.

The chitinase-like antifreeze proteins can be used: to increase field survival of plants, animals and microorganisms stopsed to sub-zero temperatures; to inhibit ice recrystallisation in biological

materials or foods; for cryopreservation and hypothermic protection

of cells, embryos, tissues etc. (particularly human platelets); and

to kill tumour cells. They are also used to inhibit initiation and

progression of diseases or spollage caused by low temperature

cryopreserved biological material.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 GPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSAA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 VSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFFGQTS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 hettggwptapdgpyswgycfngergapsdycspssgwpcapgkkyfgrgpigisynyy 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 EQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG------GGGGVASI 79
                                                                                                                                                                                                                                                                                                             New nucleic acid encoding antifreeze polypeptides from plants - particularly with chitinase activity, used to impart frost, and pathogen, resistant to plants, for preservation of foods, cells etc. and for treating tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.6%; Score 1265; DB 20; 72.7%; Pred. No. 1.3e-99;
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                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Fig 21d; 118pp; English.
                                                                                                                                                                                                                               Moffatt B,
                                                                                                                      98WO-CA00745.
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                                                                                                                                                                                           (ICEB-) ICE BIOTECH INC
                                                                                                                                                                                                                                                                  WPI; 1999-153795/13.
N-PSDB; AAX24889.
                                                                                                                                                                                                                                Hew C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 AA;
                                                  W09906565-A2
                                                                                                                       31-JUL-1998;
                                                                                                                                                           31-JUL-1997;
                                                                                                                                                                                                                                Griffith M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216;
                                                                                      11-FEB-1999
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ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT
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298 rycdilgvsyganldcysg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1995-067090/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 AA;
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                                                                                                                                                                                                                                     Rice chitinase.
                                                                                                                                                                                                                                                                                                               Oryza sativa.
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                                                                                                                                                                                                                                                                                                                                                                                                   16-JUL-1993;
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Matches 221;
                                                                                                                                                                                                                                                                                                                                                         26-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                        AAR67969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                       AAR67969
                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                  g
                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence given is encoded by the rice chitinase gene. The promoter region of this gene (see AAQ11407) is responsive to physical and/or biological stress. The pattern of expression of this protein in mature plants is characteristic. There is a low level of expression in autre laves, a moderate level in plant stems and the highest level in roots and the male and female parts of the plant. The chitinase promoter sequence may be linked to a reporter gene for expression in mono- or dicotyledon plants. Expression of this reporter gene may be used to study patterns of development and controlled expression of plant defence genes and selectable genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQCT-----GCGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARGITGDLDTRKREVAAFFGQISHETIGGWPIAPDGPFSWGYCFKQEQ-GSPPSYCDQS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGFRCQ 63
                                                                                                                                                                              Location/Qualifiers
123..323
/note= "Region conserved between class I and class
II chitinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is
                                                                                                              Promoter; region; rice; chitinase; physical; biological; stress; leaves; stems; roots; male; female; reporter; monocotyledon; dicotyledon; development; plant; defence; selectable; genes.
                                                                                                                                                                                                                                                                                                                                                                                                  DNA fragment contg. chitinase gene and its regulatory region responsive to mature plant stress and has low level expression leaves, moderate level expression in stem and high level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1230; DB 13
Pred. No. 1.4e-96;
1; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 33-34; 45pp; English.
                                                                                                                                                                                                                                                                                                                            (SALK ) SALK INST BIOLOGICAL STUDIES.
                          AAR29019 standard; Protein; 336 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.68;
69.38;
                                                                                                                                                                                                                                                                                 92WO-US04282.
                                                                                                                                                                                                                                                                                                      91US-0704288
                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                           RCH10 chitinase protein.
                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-415785/50.
N-PSDB; AAQ31407.
                                                                                                                                                                                                                                                                                                                                                                                                                                       expression in roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 AA;
                                                                                                                                                                                                                                                                                                                                                 zhu Q;
                                                                                                                                                                                                                                                                                21-MAY-1992;
                                                                                                                                                           Oryza sativa
                                                                                                                                                                                                                                                                                                      22-MAY-1991;
                                                                    20-APR-1993
                                                                                                                                                                                                                                      W09220807-A.
                                                                                                                                                                                                                                                            26-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                AAR29019;
                                                                                                                                                                                                                                                                                                                                                 Lamb CJ,
                                                                                                                                                                                Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                AAR29019
      RESULT
                             Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _{\Omega}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qγ
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and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 pqspkpscnavatgqwtpsaddqragrvpgygvitniingglecghgeddriadrigfgk 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LEARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TQSNKPSCHDVITGLWTPIARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Sphi fragment of rice chitinase RCH10 gene (given in AA081346) an alfalfa beta-1,3-glucanase coding sequence (AAQ81347) were incorporated into vectors for co-expression in transgenic tobacco, resulting in improved resistance to Cercospora nicotinae and
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic plants contg. several plant defence associated proteins - have increased resistance to plant pathogens when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chitinase; transgenic plant; disease resistance;
crop improvement; tobacco; Nicotiana tabacum; plant defense;
fungus pathogen; Cercospora nicotinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.6%; Score 1230; DB 16;
69.3%; Pred. No. 1.4e-96;
ive 31; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thanatephorus cucumeris fungal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 31-32; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhu Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                           AAR67969 standard; Protein; 336 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         grown in crops as a food source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maher EA,
                                                                                                                                                                                    295 RYCDIFGIGYGNNLDCYNQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-0093372.
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LRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP440304-A.
                                                                                                                                                                                                                                                                                                                                                                                                         AAR13275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UYLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fungal
                                                                                                                   116
                                                                                                                                                                         175
                                                                                                                                                                                                    178
                                                                                                                                                                                                                               235
                                                                                                                                                                                                                                                                                                              298
                                                                                                                                                                                                                                                                                                                                                                   AAR13275
                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                  g
                                                                                                                                                                                                                               δλ
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                                                                                                                                                                                                                                                                                   QΥ
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                                    a
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                                                                                                                    δž
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a chitinase designated RCH10. The specification describes chimeric receptors which are used for modulating plant responses to pathogens. The receptors comprise a heterologous extracellular domain (e.g. from a Bril protein or RCH10 protein) and a kinase domain (e.g. from disease resistance protein Xall) rice Xall gene is a member of disease resistance protein Xall. The Xall when Xall is present in a transgenic plant, it confers resistance to Amathomonas spp. The plant receptors containing heterologous domains are useful for modulating plant responses to pathogens including viruses, bacteria, nematodes, fungi or insects. The nucleic acids can be used to confer desired traits on essentially any plant.
                                                                                                                                                                                                                                                                                                                                                                    Disease resistance protein; Xa21; RKK gene; transgenic plant; chitinase; Xanthomonas; plant pathogen; Bril protein; RCH10 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric plant receptors comprising a polynucleotide encoding a RRK receptor containing a heterologous extracellular domain and a kinase domain from a Xa21 polypeptide, useful for modulating plant responses
                                                   234
                                                                                                          294
                                                                                                                        PAFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS
                                                                                                          235 IQSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK
                                                    175 ADWPCAPCKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT
                                                                 sequence of a rice chitinase designated RCH10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ľ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 45-46; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SALK INST BIOLOGICAL STUDIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lamb C,
                                                                                                                                                                                                                                                              AAB67444 standard; Protein; 336 AA
                                                                                                                                                                                           rycdilgvsyganldcysq 316
                                                                                                                                                                  RYCDIFGIGYGNNLDCYNQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US20714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0363313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chory J,
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA.
(SALK ) SALK INST BIOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-159858/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ronald P, He Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAF54983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200109283-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-1999;
                                                                                                                                                                                                                                                                                                                    15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-2001
                                                                                                                                                                                                                                                                                                                                               Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                         AAB67444;
                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sp.
                                                                                                                                                                  295
                                                                                                                                                                                           298
     116
                                                                                                                                                                                                                                                   AAB67444
                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                            g
                                                                                                                                                                  Qγ
                                                          Óγ
                                                                                   g
                                                                                                              22
                               qq
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The sequence from which this amino acid was deduced was isolated from a N.tabacum cDNA library following screening with a partial tobacco intracellular chitinase clone. The protein sequence appears twice in the specification but in one (not the one given in this
57
                                    TQSNKPSCHDVIIGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK
                                                                  PARGITGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS
                                                                                                               ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT
1 mralavvamvarpflaaav---haeqcgsqaggavcpnclccsqfgwcgstsdycgagcq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plants with improved resistance to pathogenic fungi - contains chitinase and/or beta-1,3-glucanase genes modified for over-expression targetted to apoplasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roekel
JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Van
Bol
                                                                                                                                                                                                                                                                                                                                                                                                                                                1..23
/label= signal peptide
24.324
/label= intracellular chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meulenhoff EJ,
Woloshuk CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                             AAR13275 standard; Protein; 324 AA.
                                                                                                                                                                                                                                                                                                                                                                                       resistance; phytopathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Fig 2; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                Tobacco intracellular chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vloemans AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Melchers LS,
                                                                                                                                                                                                             295 RYCDIFGIGYGNNLDCYNQ 313
                                                                                                                                                                                                                            RIJKSUNIV TE LEIDEN
                                                                                                                                                                                                                                                                                                                                                                                                              Nicotiana tabacum Samsun NN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91EP-0200191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90NL-0000222
                                                                                                                                                                                                                                                                                                                                           14-OCT-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOGE-) MOGEN INT NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-232019/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sela-Buurlage MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ12898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cornelissen BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-1990;
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3;

Gaps

12;

Length 336; Indels

68.68; Score 1230; DB 22; 69.38; Pred. No. 1.4e-96; Live 31; Mismatches 55;

Query Match
Best Local Similarity 69.3%
Matches 221; Conservative

Tue May

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WPI; 1997-479536/44.
N-PSDB; AAT89952.
                                                                                                                                                                              Similarity
                                                                                                                                              324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6087560-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUL-2000.
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                                                                                                                                                                                Local Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB07513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                 Sequence
                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                      29
                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    AAB07513
                                                                                                                                                                                                                                                                                                                                                                                                                                             q
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     5
                                                                                                                                                                                                          185 YYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHD 244
                                                                                                                                                                                                                                245 VITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGY 304
                                                                                                                                                                            125 DTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQ 184
                                                                                                                                   67 IG--CGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDL 124
                                                                                     Gaps
                                                                                                            file), the Leu codons at positions -23, -21, -15, -12, -11, -8, -7, -6, -5 and plus 16, 52, 65, 137, 176, 177, 182, 195, 228, 242, 266, 274, 286 are translated as Ile.
See AA012897-Q12900.
                                                                                                                                                                                                                                                                                                                                                                                      antifungal; transgenic plant; synergism; tobacco.
                                                                                                    CATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQC
                                                                     DB 12; Length 324;
                                                                                     .,
                                                                    ; Score 1177.5; DB 12; Lengt.
; Pred. No. 3.9e-92;
45; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melchers LS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cornelissen BJC, Linthorst HJM, Melcher
Ff EJS, Sela-buurlage MB, Van ROEKEL JSC;
AA, Woloshuk CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "intracellular protein"
                                                                                                                                                                                                                                                                                                                                                                        Nicotiana sp. intracellular chitinase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                           l..23
/label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                           AAW31297 standard; Protein; 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0047413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-0647B31
                                                                       65.7%;
64.2%;
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                         Intracellular chitinase;
beta-1,3-glucanase gene;
                                                                                                                                                                                                                                                                    305 GNNLDCYNQLSFNVGL 320
                                                                                        Conservative
                                                                                                                                                                                                                                                                              |:|||| || || || || || 304 gdnldcgnqrsfgngl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOGE-) MOGEN INT NV
                                                                         Query Match
Best Local Similarity
                                                  324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vloemans AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                    Nicotiana sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5670706-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bol JF, Co
Meulenhoff
                                                                                                                                                                                                                                                                                                                                                           11-MAR-1998
                                                                                          203;
                                                                                                                                                                                                                                                                                                                                             AAW31297
                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                   Sequence
                                                                                                                                                                                                                                                                                                             6
                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                    AAW31297
                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                           Db
                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                      δž
                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                      QY
                                                                                                                       q
                                                                                                                                        δλ
                                                                                                                                                        Q
                                                                                                                                                                       QΥ
                                                                                                                                                                                      QQ
                                                                                                                                                                                                       QY
           8888%8
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2;
                                                                                                           This sequence represents an intracellular chitinase which is used to construct a transgenic plant in a novel method to produce plants resistant to fungal attack. Such transgenic plants expressing an intracellular plant chitinase gene and a plant beta-1,3-glucanase gene within its tissues are predicted to exhibit improved resistance to pathogenic fungi. Such genes should be operably linked to promoters and terminators and optionally a gene encoding a selectable or screenable trait. Plants that overexpress the chitinase and glucanase genes exhibit a synergistic antifungal effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 VITGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYRRYCDIFGIGY 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIRKREVAAFFGQISHETIGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TG--CGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 YYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CATAVLAVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQC
                                                                                                      an intracellular chitinase which is used
                                                                                                                                                                                                                                                                                                                                                                                                            Length 324;
Fungus-resistant transgenic plants - containing genes encoding intracellular chitinase and beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chitinase; transgenic plant; beta-1,3-glucanase; antifungal; plant resistance; pathogenic fungi; fungal resistant plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of an extracellular chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                              DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                  Score 1177.5; DB 18;
Pred. No. 3.9e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..23
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB07513 standard; Protein; 324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
                                                                     Example 4; Fig 2; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                   65.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|||| || || || 304 gdnldcgnqrsfgngl 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 GNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Nicotiana tabacum L. c.v. Havana 425

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Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                               The present sequence represents an extracellular chitinase. The specification describes transgenic plants which express a chitinase gene and a glucanase gene. The expression of the chitinase and beta-1, 3-glucanase genes produces an antifungal effect. The transgenic plants are useful for improving plant resistance to pathogenic fungi. The recombinant polynucleotides and the process are useful for producing fungal resistant plants.
                                                                                                                                                                                                      New transgenic plants expressing chitinase and glucanase have improved resistance against pathogenic fungi, particularly against Alternaria alternata or Fusarium oxysporum f. sp. lycopersici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 VITGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGY 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 tarkrelaalfaqtshettggwatapdgpyawgycwlreqospgdyctpsgqwpcapgrk 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 TG--CGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                Melchers LS, Meulenhoff EJS, Sela-buurlage MB;
oshuk CP, Bol JF, Linthorst HJM, Van Roekel JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ckftalssllfsllllsasaeqcgsqaggarcasglccskfgwcgntndycgpgncqsqc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 DTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vacuole, targetting; chitinase; glucanase; signal; resistance; pharmaceutical; hormones; expression; secretion; extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.7%; Score 1177.5; DB 64.2%; Pred. No. 3.9e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Basic chitinase 48 from clone lambdaCHN17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä.
                                                                                                                                                                                                                                                                       Example 4; Fig 2A-B; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR15841 standard; Protein; 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
                              93US-0047413.
91US-0647831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
97US-0801563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 GNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1:|||| || || || || 304 gdnldcgnqrsfgngl 319
                                                                                                                                   Woloshuk CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity 64.2
203; Conservative
                                                                          RIJKSUNIV LEIDEN
                                                                                        MOGEN INT NV
                                                                                                                                                                 WPI; 2000-498214/44.
N-PSDB; AAA58910.
                                                                                                                      Cornelissen BJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-1992
                                                                                                                                      Vloemans AA,
 18-FEB-1997;
                               19-APR-1993;
                                              29-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR15841;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                            (UYLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
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IID AAR1

AC AAR1

XX AAR1

XX I9-M

XX BASI

XX VACU

KW VACU

XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
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240 PSCHDVITGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APGKQYYGRGPIQLTHNYNYGPAGRAIGYDLLNNPDLVATDPTVAFKTAIWFWMTTQSNK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 TG-----CGGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 pggptptpptppgggdlgsiisssmfdqmlkhrndnacggkgfysynafinaarsfpgfg 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 TIGDLDTRKREVAAFFGQTSHETIGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Attachment of the signal peptide ensures occlusion of expressed prod. in the vacuole while elimination of the signal peptide from a sequence normally contg. it ensures that the expressed product is secreted into the extracellular space, rather than retained in the vacuole. Recombinant DNA may contain a structural gene which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 CATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the vacuole. Recombinant DNA may contain a structural gene which protects the plant, e.g. resistance to pathogens, herbicides, insecticides, biocides, environmental stress, etc.; leads to increased prodn. of proteins, carbohydrates, etc.; or encodes for pharmaceuticals such as hormones or immunommodulators. See also AAQ15146-50 and AAQ15330-35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.
                                                                                                                                                                                                                                                                                                                                                                           DNA sequence encoding vacuole targetting peptide - esp. signal region of tobacco chitinase or glucanase gene, and derived recombinant DNA, vectors, etc. functional in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.3%; Score 1170; DB 12; Length 329;
63.2%; Pred. No. 1.7e-91;
.ive 44; Mismatches 66; Indels 9
                                                                                                                  318..329
/label= sig_peptide
/note= "used as vacuole targetting peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 64-68; 81pp; English.
                                                                           /label= exon2-prod.
200.329
/label= exon3_prod.
318.329
                      Location/Qualifiers
                                                   exon1_prod
                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 FGIGYGNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                               Ryals
                                                                                                                                                                                                                               91EP-0810430
                                                                                                                                                                                                                                                       90CH-0002007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203; Conservative
                                                               149..199
                                                /label=
                                                                                                                                                                                                                                                                                                               Nauhaus JM,
                                                                                                                                                                                                                                                                                      (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                           WPI; 1991-371028/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 AA;
                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ15147
                                                                                                                                                                                                                               06-JUN-1991;
                                                                                                                                                                                                                                                          15-JUN-1990;
                                                                                                                                                                             EP462065-A.
                                                                                                                                                                                                                                                                                                                 Boller T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                      Peptide
                            Key
Region
                                                                                             Region
                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
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QC
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GYGVITINVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Shinshi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-088356/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 204; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     See also AAQ11094
                                                                                                                                                                                                                                                         Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ11093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        level
                                                                                                                                                                                                                                                                                                                                               10-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                           13-SEP-1989;
                                                                                                                                                                  30-MAY-1991
                                                                                                                                                                                                                                                                                                                   27-MAR-1991
                                                                                                                                                                                                                                                                                     EP418695-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a high
                                                                                                                                                                                                                                                                                                                                                                                                                                     Meins F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                    AAR11305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
      264
                                                                              RESULT
                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the pumpkin chitinase. Chitinase is an enzyme decomposing chitin (not present in plant cell membranes) found in the cell membranes of fungi. Plants have this enzyme to protect themselves from pathogenic fungi. Plants have this enzyme to protect themselves from being infected with pathogenic fungi, and the chitinase gene can be introduced into plants to improve their resistance to diseases caused by fungi. As the amino acid sequence of the chitinase does not have any region to be cleaved by ubiquitous peptidases in cells, the chitinase produced by genetic recombination technology works for various host cells and serves for plant immunity to confer disease resistance on plants as
                                                                                                                                                                                                             Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase; fungal cell membrane; pathogenic fungus; disease resistance; chitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGPAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFERFLIHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFFGQTSHETT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 eqcgrqangalcpnrlccsqfgwcgntdeycknncqsqctppstgggggggggsvgsinea 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 EQCGSQAGGAKCADCLCCSQFGFCGTTSDXCGPRCQSQC----TGCGGGGGGVASIVSRD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSAAGRVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 18; Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chitinase derived from pumpkin - used to protect plants against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.9%; Score 1163.5; DB 18; Lengt
69.6%; Pred. No. 5.3e-91;
ive 30; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           ZH SEKIYU SANGYO KASSEIKA CENTER
                                                                                               A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 2; 36pp; Japanese.
                                                                                             AAW24554 standard; Protein; 292
      95JP-0347367.
                                                                                                                                                                                                                                                                                                                                                                              95JP-0347367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT79940, AAT79941.
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                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-380170/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 204; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathogenic fungi
                                                                                                                                                                                                                                                           Cucurbita pepo.
                                                                                                                                                                                                                                                                                                                                                                                                             (NIHA ) JAPAN
                                                                                                                                                                                                                                                                                        JP09163987-A
                                                                                                                                                                                                                                                                                                                                                14-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                              14-DEC-1995;
                                                                                                                                                                                                                                                                                                                      24-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serves
host.
                                                                                                                                                       10-OCT-1997
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                                                                                                                         AAW24554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             (SEKI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
                                                                 RESULT 1
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TG-----CGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGDIDIRKREVAAFFGQISHETIGGWPIAPDGPFSWGYCFKQEQGSPPSYC-DQSADWP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAPG-KQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CATAVLAVALAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This recombinant tobacco chitinase gene prod. is encoded by a genomic clone, lambda CHN17 which comprises 3 exons and has 5'- and 3'- untranslated regions. A fragment (claimed) from the 5'-untranslated regions. A fragment (claimed) from pression of foreign genes in transgenic plants. The fragment is linked to a foreign gene, eg chitinase or glucanase gene via a spacer and is also linked to regulatory sequences. The resultant DNA construct is used to transform plant cells, eg tomato or tobacco, which subsequently produce the gene prod.
240 gygvitniingglecgrgadsrvadrigfykrycdllgigygnnldcnngrsf 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA regulatory sequence from new tobacco chitinase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used to increase expression of foreign genes in transgenic
plants, partic for improving resistance to pathogens etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                  Plant chitinase; transgenic plants; pathogen resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65;
                                                                                                                                                                                                                                                                                                                            Chitinase encoded by genomic clone lambda CHN17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1161; DB :
Pred. No. 1e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                               A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; page 44; 65pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuhaus J-M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                        AAR11305
ID AAR11305 standard; Protein; 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.8%;
63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90EP-0117389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89CH-0003334.
                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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á qq δ d Ω g à VAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGP 190

IQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLW

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251 TPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDC
                                                                                                                                        311 YNQLSFNVGL 320
                                                                                                                                                                                                   303 Yngrpfgngl 312
                                                                                    191
                                        131
                                                                                                                                                                                                                                       RESULT
                                                              q
                                                                                    QΥ
                                                                                                          g
                                                                                                                                  Qγ
                                                                                                                                                       g
                                                                                                                                                                              Q\underline{\gamma}
                                                                                                                                                                                                  Ω
                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is encoded by the CDNA clone pHS2, and represents a protein having chitinase-activity derived from american elm. This protein inhibits the fungus Ophiostoma ulmi, the causative agent of dutch elm disease. The clone pHS2 may be used to transform E. coli cells for the recombinant production of the chitinase-like protein. The protein may be used in a composition to inhibit fungal infection of elm trees.
         184 capgrrkyfgrgpiqishnynygpcgraigvdllnnpdlvatdpvisfksalwfwmtpgs 243
                                            297
                                NKPSCHDVITGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated chitinase gene derived from an American elm - used to obtain prods, for inhibiting fungal infection of plants
                                                                                                                                                                                                                                                  ; american elm; fungus; Ophiostoma ulmi; coli; chitinase-like protein;
                                                                                                                                                                                                                                                                                                                                                                   "Mature chitinase-like protein"
                                                                                                                                                                                                                                                                                                                                      /note= "signal peptide" 22..317 /note= "Mature chitinas
                                                                                                                                                                                                                               American elm chitínase-like protein.
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                            AAW00186 standard; Protein; 317 AA
                                                                              298 DIFGIGYGNNLDCYNQLSFNVGL 320
                                                                                            304 silgvspgdnldcgnqrsfgngl 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0286020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNMS ) UNIV MICHIGAN STATE
                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sticklen MB;
                                                                                                                                                                                                                                                      chitinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 1; 12pp;
                                                                                                                                                                                                                                                                disease; E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-353879/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT33325
                                                                                                                                                                                                                                                                              fungal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                       04-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-AUG-1994;
                                                                                                                                                                                                                                                                                                  American elm
                                                                                                                                                                                                                                                      Clone pHS2;
dutch elm di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hajela RK,
                                                                                                                                                                                                                                                                                                                                                                                           US5539095-A
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                                                                                                                                                                                                         18-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                    AAW00186;
                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                   AAW00186
                                                                                                                                                                          QQ
                                                                                 Óλ
                                     Q_{\overline{Y}}
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The inventors claim a new recombinant gene which codes for a protein with encochitinase activity, or its precursor (see AAQ21007). The coding part of the gene contains at least the 5' part of DNA for tomato enzyme (DNA can be genomic or cDNA, but at least one intron is prefigresent). The recombinant gene includes the 35s promoter of cauliflower mosaic virus plus the terminator from the nopaline synthase gene of Agrobacterium tumefaciens.
                                                                                                       Pest-resistant plant; transformed plant; fungi; insect; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant protein with endo chitinase activity - also encoding it and plants which express it, resistant to fungi, insects, bacteria and nematodes.
                                                                                                                                                                                                                                                                                                                                                                 Toppan A;
                                                                                                                                                                                                                                                                                                                                                                 Pignard A,
                                                                                      endochitinase procursor,
                                                                                                                                                                 Location/Qualifiers
                AAR20822 standard; Protein; 328 AA.
                                                                                                                                                                              1..24
/label= signal
25..69
/label= cleavage
                                                                                                                                                                                                                                                                                                                                                                  Leguay JJ,
                                                                                                                                                                                                                                                                                                                                (SNFI ) SANOFI SA.
(ERAP ) SOC NAT ELF AQUITAINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 4; 82pp; French
                                                                                                                                                                                                                                                                                                          90FR-0009460.
                                                                                                                                                                                                                                                                                   91WO-FR00607
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                 Grison R,
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-064950/08.
                                                                                                                                               tobacco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ21193
                                                                                                                                                                                                                                                                                     24-JUL-1991;
                                                                                                                                                                                                                                                                                                           24-JUL-1990;
                                                                                                                                                                                                                                                              06-FEB-1992.
                                                                                                                                                                                                                                        WO9201792-A.
                                                               16-MAY-1992
                                                                                      Sequence of
                                                                                                                                               romato and
                                                                                                                                                                                                                                                                                                                                                                  Subois M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                         nematode
                                          AAR20822
                                                                                                                                                                              Peptide
                                                                                                                                                                                                     Peptide
15
         AAR20822
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Indels

DB 17; Length 317;

Score 1160; DB 17 Pred. No. 1.2e-90; Mismatches

64.7%; 65.8%;

33;

Conservative

204;

Similarity

Local

Best Loca Matches

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Query Match

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÷.
                                                                                                                                                                       120 TIGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPC 179
                                                                                                               66 CTGCGGG-----GGGVASIVSRDLFERFILLHRNDAACLAR-GFYTYDAFLAAAGAFPAFG 119
                                                                             7 RCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQEGFCGTTSDYCGP-RCQSQ 65
                                            7; Gaps
DB 13; Length 328;
                  66; Indels
Query Match
63.8%; Score 1142.5; DB
Best Local Similarity 60.4%; Pred. No. 3.7e-89;
Matches 194; Conservative 54; Mismatches 66
                                                                                                                                                                                                              300 FGIGYGNNLDCYNQLSFNVGL 320
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Search completed: May 3, 2002, 18:30:30 Job time: 7549 sec

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4 LRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQ
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                                                                                                                        3, 2002, 18:43:02 ; Search time 79.44 Seconds (without alignments) 91.498 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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Sequence 11,
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                                                                                                                                                                                                                                                    1 MSTERARCATAVLAVVLAAA.....rGNNEDCYNQESFNVGLAAQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/pcata/2/iaa/pcata/2/iaa/pcata/2/iaa/pcata/2/iaa/pcata/2/iaa/pcata/2/iaa/pcata/2/iaa/pcata/2/iaa/pcata/2/iaa/pcata/2/iaa/pcata/2/iaa/pcata/2/iaa/pcata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/acata/aca
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-047-413-11

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US-08-229-050-11

US-08-229-050-11

US-07-791-931-6

US-08-379-259-6

US-08-379-259-6

US-07-791-931-7

US-07-791-931-7

US-07-791-931-5

US-08-379-259-9

US-08-379-259-9

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Sequence 8, Appli
Patent No. 5187262
Sequence 14, Appl
                                                                                                             App]
                                                                                                                                                                                                                                                                                                                                             APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: LAMB, QUA
TITLE OF INVENTION: ELEMENTS
TITLE OF INVENTION: ELEMENTS
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STREET: California
COUNTRY: United States
ZIP: 90071-2921
                                                           Sequence 2, P
Sequence 4, P
Sequence 8, P
Sequence 4, P
Sequence 37, Sequence 35,
                                                                                                                                      Sequence 3
Sequence 1
Sequence 1
                       Sequence
Sequence
                                                 Sequence
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MEDIUM TYPE: Floppy disk
GOMPOTER: IBM PC compatible
OPPRATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 8000
US-08-047-413-9

US-08-229-050-9

US-08-162-475A-5

US-08-162-475A-2

US-08-162-475A-2

US-08-162-475A-2

US-07-791-931-9

US-07-791-931-8

US-07-791-931-8

US-07-791-931-8

US-08-329-799-35

US-08-329-799-35
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US-07-704-288C-14
                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen 31,192
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
TELECHONICATION INFORMATION:
TELEPHONE: (619) 546-4337
TELEFAX: (619) 546-4337
                                                                                                                                                                                                                                                                                                  0.0077-704-288C-3
0.05-07-704-288C-3
; Sequence 3, Application US/07704288C
; Patent No. 5399680
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SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-07-704-288C-3
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      TOPOLOGY:
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3,

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                           295 RYCDIFGIGYGNNLDCYNQ 313
                                                                                                                                                                                                                                                                                                   298 RYCDILGVSYGANLDCYSQ 316
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amino acid
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Best Local Similarity 69.3%
Matches 221; Conservative
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CORRESPONDENCE ADDRESS:
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US-08-379-259-3
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CITY: LA
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                                                                                                                                                                                                                                  238 PQSPKPSCNAVATGQWTPSADDQRAGRVPGYGYJTNIINGGLECGHGEDDRIADRIGFYK 297
                      175 ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWWT 234
                                                                                         64 SQCT-----GCGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAF
                                                                      116 PAFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ-GSPFSYCDQS
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Patent No. 5530187
GENERAL INFORMATION:
APPLICANT: Lamb, Christopher J.
APPLICANT: Zhu, Qun
APPLICANT: Apher, Elleen A.
APPLICANT: Dixon, Richard A.
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STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1230; DB 1;
Pred. No. 1.6e-103;
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FILING DATE: 16-JUL-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31,192
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TELEPHONE: 619-546-4737
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69.3%;
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS: ADDRESSEE: Pretty, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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Best Local Similarity
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CLASSIFICATION:
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US-08-093-372-2
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STATE:
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                                                                                                                                                                                                                                                                                235 TQSNKPSCHDVITGIWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                    175 ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-08-379-259-3
US-08-379-259-3
Sequence 3, Application US/08379259
Patent No. 5695939
Patent No. 5695930
Patent No. 5
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69.3%; Pred. No. 1.6e-103;
Live 31; Mismatches 55;
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JULYWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OR/JTC
FILING DATE:
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APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31,8899
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US-08-229-050-11
               TOPOLOGY:
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APPLICANT: Welchers, Leo S.
APPLICANT: van Roekel, Jercen S.C.
APPLICANT: van Roekel, Jercen S.C.
APPLICANT: Sela-Buurlage, Marianne B.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Moloshuk, Charles P.
APPLICANT: Moloshuk, Charles P.
APPLICANT: Moloshuk, Charles P.
APPLICANT: Bilthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         116 PAFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS 174
                                                                                                                                                          175 ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT 234
                                                                                                                                                                                                                          235 IQSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK 294
                                                                  64 SQCT-----GCGGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAF 115
                                                                                      63
                                   23
   4 LEARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQ
                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/047,413
FILING DATE: 000
CLASSIFICATION: 000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDITION OF STREET STREET STREET STREET: 755 Page Mill Road CITY: Palo Alto STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 07/647,831
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Patent No. 5670706
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IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19-APR-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 295 RYCDIFGIGYGNNLDCYNQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Murashige, Kate H
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US-08-047-413-11
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APPLICANT: Bol, John F. APPLICANT: Linthorst, Hubertus J.M. APPLICANT: Linthorst, Hubertus J.M. TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT TITLE OF INVENTION: POLYNUCLECTIDES FOR USE THEREIN NUMBER OF SEQUENCES: 17
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                                                                                                                                                                                                                                                                                               67 TG--CGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDL 124
                                                                                                                                                                                                                                                                                                                            64 PGGPIPPGGGDLGSIISSSWEDQMLKHRNDNACQGKGFYSYNAFINAARSFPGFGTSGDT 123
                                                                                                                                                                                                                                                                                                                                                                                              125 DTRKREVAAFFGQTSHEITGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQ 184
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                                                                                                                                                                                                8 CATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFC
                                                                                                                                                                                                                                       4 CKFTALSSILFSILLISASABQCGSQAGGARCASGLCCSKFGW
                                                                                              65.7%; Score 1177.5; DB 64.2%; Pred. No. 8.4e-99; iive 45; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cornelissen, Bernardus J.C. APPLICANT: Melchers, Leo S. APPLICANT: Mellenbff, Elisabeth J.S. APPLICANT: van Roekel, Jeroen S.C. APPLICANT: Sela-Buurlage, Marianne B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,831
FILING DAIE: 29-URN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/229,050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Meulenhoff, Elisabeth J
APPLICANT: van Roekel, Jeroen S.C.
APPLICANT: Sela-Buurlage, Marianne
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
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STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08229050
Patent No. 6066491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                         Best Local Similarity 64.2% Matches 203; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
, MOLECULE TYPE: protein US-08-047-413-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: California
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Sequence 11, Application US/08801563
Patent No. 6087560
GENERAL INFORMATION:
APPLICANT: Cornelissen, Bernardus J.C.
APPLICANT: Welchers, Leo S.
APPLICANT: van Roekel, Jeroen S.C.
APPLICANT: van Roekel, Jeroen S.C.
APPLICANT: van Roekel, Jeroen S.C.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Bol, John F.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            3
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                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                    Length 324;
                                                                                                                                                                                                                                                                         65.7%; Score 1177.5; DB 3; Lengtl:
64.2%; Pred. No. 8.4e-99;
tive 45; Mismatches 65; Indels
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
RELECOMOCKET NUMBER: 24615-20022.00
TELECOMMUNICATION INFORMATION:
TELERPAX: 415-813-5600
TELEFRAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Morrison & Foerster
755 Page Mill Road
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IBM PC compatible
                                                                                      TELEKX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                  Conservative
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STREET: 755 ...
CITY: Palo Alto
                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-229-050-11
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Matches 203; Conserv
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185 YYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHD 244
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PC-DOS/MS-DOS
n Release #1.0, Version #1.25
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APPLICANT: RAIGHAL, NATASHA V.

TITLE OF INVENTION: Nettle Lectin CDNA
FILE REPERENCE: MSO 4.1-11 4

CURRENT APPLICATION NUMBER: US/07/791,931C

CURRENT FILING DATE: 1991-11-12

NUMBER OF SEQ ID NOS: 19
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APPLICATION NUMBER: US 08/047,
FILING DATE: 19-APR-1993
APPLICATION NUMBER: US 07/647,
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MULSALIGE, KATE H.
REGISTRATION NUMBER: 29,595
REFERENCE/DOCKET NUMBER: 2461;
TELECOMMUNICATION:
TELECOMMUNICATION:
TELETAN: 415-494-0792
TELETA: 706141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 324 amino acids
amino acid
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Best Local Similarity 64.2%
Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                  SULTWARE: PATENTIN RECURRENT APPLICATION DATA APPLICATION NUMBER: U FILING DATE:

CLASSIFICATION: 800
PRIOP ADDITION: ADDITION
                                                                                                                                    DATA
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OPERATING SYSTEM:
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LENGTH: 310
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TITLE OF INVENTION: BLEMENTS
TITLE OF INVENTION: BLEMENTS
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                  57 SSMFDQMLKHRNDNACQGKGFYSXNAFINAARSFPGFGTSGDTTARKKEIAAFFAQTSHE 126
                                                                                                                                                                                                                                                             TTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGP 201
                                                                                                                                                                                                                                                                                                                                    AGRAIGVDLLNNPDLYATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSAAGR 261
                                                                                                                                                                                       82 RDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFFGQTSHE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                  25 ATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQCTG--CGGGGGGVASIVS
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                                               Length 310;
                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                   DB 4;
                                                 65.7%; Score 1176.5; DB 67.2%; Pred. No. 9.8e-99;
                                                                                     41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/07/704,288C
22-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: F31 8899
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/07704288C Patent No. 5399680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
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FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RY: United States 90071-2921
                                                   Query Match
Best Local Similarity 67.28
Matches 201; Conservative
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid STRANDEDNESS: unl
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US-07-704-288C-6
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US-07-791-931-6
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82 RDLFERFILLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFFGQTSHE 141
                                                                                                                                   TTGGWPTAPDGFFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGP 201
                                                                                                                                                                                                    202 AGRAIGYDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSAAGR 261
               Gaps
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                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
APPLICANT: ZHU, QUN
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/379,259 FILING DATE:
; Pred. No. 7.1e-98; 41; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DAWS:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: P31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                           7.508-379-259-6
; Sequence 6, Application US/08379259
; Patent No. 5695939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31,192
   67.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 amino acids
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SEQUENCE CHARACTERISTICS:
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                     Matches 201; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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       Best Local Similarity
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APPLICANT: DUBOIS, Michel
APPLICANT: GRISON, Rene
APPLICANT: GRISON, Rene
APPLICANT: LEGGRAY, Jean-Jacques
APPLICANT: PIGRAKD, Annie
APPLICANT: POPRAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                     177 WPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                             63 QSQCTGCGGG-----GGGVASIVSRDLFERFLLHRNDAACLAR-GFYTYDAFLAAAGAFP 116
                                                                                                                                                                                                                                                                          61 QSQCPGGGPGPGPVTGGDLGSV1SNSMFDQMLKHRNENSCQGKNNFYSYNAFITAARSFP 120
                                                                                                                                                                                                                                                                                                                    117 AFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSAD 176
                                                                                                                                                                                                                                                                                                                                            SNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRY 296
                                                                                                                                                     4 LRARCATAVLAVALAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RC 62
                                                                                                                                                                              7;
                                                                          Length 329;
                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: FOLEY & LARDNER STREET: King Street Station, Suite 500,1800 Diagonal STREET: Road, PO Box 299 CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.25
                                                                            DB 2;
                                                                                                                   :69
                                                                        63.7%; Score 1141.5; DB
59.9%; Pred. No. 1.5e-95;
Live 54; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION UNMER: US/07/842,165
FILING DATE: 19920501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/07842165; Patent No. 5932698; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 CDIFGIGYGNNLDCYNQLSFNVGL 320
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TELEPHONE: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13:
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(703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACIERISTICS:
                                                                                                                       Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
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  protein
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                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
; MOLECULE TYPE:
US-08-475-427-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-842-165-13
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                                                                                                                                                                                                                                                                                                              202 AGRAIGVDLINNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSAAGR 261
                                                                                                                                                                                                                                 142 TTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGP 201
                                                                                                                                                                                                                                                                                                                                                                                             262 VPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                                247 LPGFGVITNIINGGLECGRGTDSRVQDRIGFYRRYCSILGVSPGDNLDCGNQRSFGNGL 305
                                                                                       Gaps
                                                               25 ATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQCTG--CGGGGGGVASIVS 81
                           Indels
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    Pred. No. 7.1e-98;
1: Mismatches 53;
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APPLICATION NUMBER: US/08/475,427
FILING DATE: 07-001.1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/475,427
FILING DATE: 07-001.1995
APPLICATION NUMBER: US 07/842,165
FILING DATE: 01-001.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00607
FILING DATE: 21-0101.1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90 09460
FILING DATE: 24-0101.1990
ATTORNEY-AGENT INFORMATION:
NAME: BENY, SLEPPEN A.
  67.2%; Pred. No. +ive 41; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE PORM:
MEDIUM TYPE: FIDAPY disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08475427
Patent No. 5859340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GRISON, Rene
APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BENT, Stephen A. REGISTRAILON NUMBER: 29,768 REGISTRAILON NUMBER: 16 REFERENCE/DOCKET NUMBER: 16 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 13:
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APPLICANT: DUBOIS, Michel
APPLICANT: GRISON, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                           201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOPOLOGY: linear
          Best Local Similarity
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US-08-475-427-13
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LTHNYNYGPAGRAIGVDLLANNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTP 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGGG 72
                                   253 TARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYN 312
                                                     252 SSADVAARRIPGYGTVINIINGGLECGRGQDSRVODRIGFFKRYCDLLGVGYGNNLDCYS 311
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                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: PRETIY, SCHROEDER, BRUEGGEMANN & CLARK STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTY: United States
LIP: 90071-223
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA::
APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Reditar, Stephen E.
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: 31,192
                                                                                                                                                                                                                                                Sequence 9, Application US/07704288C Patent No. 5399680
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,192
REPERENCE/COCKET NUMBER: P31
FELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEPHONE: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 amino acids
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196; Conserva
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                                                                                                                     313 QLSFNVGL 320
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                                                                                                                                                                                                                                                                                                                                                                                              236
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                                                                                                                                                                                                                                                                                             QSQCTGCGGG-----GGGVASIVSRDLFERFLLHRNDAACLAR-GFYTYDAFLAAAGAFP 116
                                                                                                                                                                                                                                              237 SNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 WPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQ
                                                                                                                                                                                                                      4 LRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RC
                                                                                                                                                                                                                                                                                                                       Length 328;
                                                                                                                                            Length 329;
                                                                                                                                                                                    69; Indels
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63.6%; Pred. No. 5.3e-95;
Live 44; Mismatches 67; 1
                                                                                                                                                DB 2;
                                                                                                                                              Query Match 63.7%; Score 1141.5; DB 3. Best Local Similarity 59.9%; Pred. No. 1.5e-95; Matches 194; Conservative 54; Mismatches 69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Raikhel, Natasha V.
TITLE OF INVENTION: Nettle Lectin CDNA
FILE REPERBORS: MSJ 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/07791931C Patent No. 6133507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 CDIFGIGYGNNLDCYNQLSFNVGL 320
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Best Local Similarity 63.6%
Matches 196; Conservative
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                   : 329 amino acids
AMINO ACID
                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-842-165-13
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                     LENGTH:
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                                                                                                                  253 TARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYN 312
                                      193 LTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTP 252
124 AFLGQTSHETTGGWATAPDGPYAWGYCFVRERN--PSTCSAŢPQFPCAPGQQYYGRGPIQ 181
                                                                                                                                      242 SSADVAARRLPGYGTVTNIINGGLECGRGQDSRVQDRIGFFKRYCDLLGYGYGNNLDCYS 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 VSAALAQNCGSQGGGGKACASGQCCSKFGWCGNINDYCGSGNCQSQCPGGGPGGPGGDLG 80
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                                                             Length 328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
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Pred. No. 3.8e-94;
3; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: RAIKHA!.
TITLE OF INVENTION: Nettle Lectin CDNA
FILE REFERENCE: MSU 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3, 2002, 18:43:04
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nilarity 62.7%;
Conservative 48
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SEQ ID NO 5
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Job time: 747 sec
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Matches 190;
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US-07-791-931-5
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                                                  253 TARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYN 312
                                                                         242 SSADVAARRLPGYGTVTNIINGGLECGRGQDSRVQDRIGFFKRYCDLLGVGYGNNLDCYS 301
            182 ISWNYNYGQCGRAIGVDLLNKPDLVATDSVISFKSALWFWMTAQSPKPSSHDVITSRWTP 241
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; Pred. No. 2e-94;
42; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                              PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
FILING DATE:
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Releater: Stephen E.
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: 931 8899
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: LAMB. CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: DEFENSE
TITLE OF INVENTION: DEFENSE REGUL
TITLE OF INVENTION: DEFENSE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  Sequence 9, Application US/08379259 Patent No. 5695939
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63.6%;
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TELEFAX: (619) 546-9392
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LENGTH: 318 amino acids
TYPE: amino acid
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Matches 196; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California
COUNTRY: United States
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STREET: 444 South
CITY: Los Angeles
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TOPOLOGY: unk
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US-08-379-259-9
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GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     - protein search, using sw model
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length: 2000000000
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9 1002 55.9 264 2 \$26625 0 997 55.6 263 2 \$72528 1 988 55.1 318 2 103026 2 973 54.3 263 2 \$69184 3 969.5 54.1 336 1 \$18750 4 954 53.2 2 \$37341 5 915.5 51.1 275 2 103032	9 1002 55.9 264 2 S26625 0 997 55.6 263 2 S72528 1 973 54.3 263 2 S69184 3 969.5 54.1 336 1 S18750 4 954 53.2 246 2 S37341 5 915.5 51.1 275 2 T03032	ω	56.	340	7	548030	probable chitinase
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		5 915	51.	275	2	0303	(EC 3
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                                                                                                                                                                                                                                                        56 DYCGPRCOSOCTGCG-----GGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAF 108
                                                                                                                                                                                                                                                                                               109 LAAAGAFPAFGTTGDIDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPP 168
                                                                                                                                                                                                                                                                                                                                     169 SYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTA 228
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                             1 MSTLR-----ARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTS 55
                                                                                                                                                                                                16;
                                                                                                                                                                             Length 339;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                                                                                                                                                                                                RIGEYKRYCDIFGIGYGNNLDCYNQLSFN----VGLAAQ 323
                                                                                                                                                                            Query Match 74.2%; Score 1330; DB 2; Best Local Similarity 71.4%; Pred. No. 1.4e-94; Matches 242; Conservative 29; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                                                                                                       Db
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A. Experimental source: cv. NK1558
C. Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; C. Superfamily: lectin-related plant chitinase; hevein chitin-binding formation c; Reywords: glycosidase; hydrolase; polysaccharide degradation
F. 19/Domain: signal sequence #status predicted <SIG>F:20-318/Product: chitnase #status predicted <AMA1>F:20-60/Domain: hevein chitin-binding domain homology <HCB>F:80-318/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          barley chitinase genomic clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Hordeum vulgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 SHAVITGQWSPSGTDRAAGRVPGFGVITNIVNGGIECGHGQDSRVADRIGFYKRYCDILG 302
                                                                                                                                                                                                    A; Residues: 1-318 <1GN>
A; Cross-references: EMBL:U02287; NID:9495304; PIDN:AAA18586.1; PID:9495305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSTPVTPTPSGGGGGSSIVSRALFDRMLLHRNDGACQAKGFYTYDAFVAAASAFRGFGTT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 GDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 GKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 CHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GGGGVASIVSRDLFERFILHRNDAACLARGFYTYDAFLAAAGAFPAFGTT 121
                                                                      DSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLS 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG 71
                                   VASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFF
                                                                                                                                                                 GQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTH
                                                                                                                                                                                                                                                                                                  NYNYGPAGRAIGYDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTAR
                                                                                                                                                                                                                                                                                                                                     Length 318;
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Pred. No. 4.4e-92;
7; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable chitinase (EC 3.2.1.14) precursor - barley C; Species: Hordeum vulgare (barley)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: T04403
S; Ignatius, S.M.J; Huang, J; Muthukrishnan, S.
submitted to the EMBL Data Library, September 1993
A; Description: Isolation and characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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74.08;
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Matches 233; Conserv
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chitinase (EC 3.2.1.14) - rice
G;Species: Orgza sativa (rice)
G;Species: Orgza sativa (rice)
G;Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: 840414
R;Nishizawa, Y.
B;Nishizawa, Y.
B;Nishizawa, Y.
B;Nishizawa, Y.
B;Neference number: 840414
A;Recession: 840414
A;Recession: 840414
A;Necession: 840414
A;Necession: 840414
A;Necession: 840414
A;Necession: 1-340
A;Necession: 
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chitinase (EC 3.2.1.14) a - rye
c; Species: Secale cereale (rye)
c; Species: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999
C; Accession: JG2071
R; Yamagami, T.; Funatsu, G.
Bhosci. Biotechnol. Biotchem. 58, 322-329, 1994
A; Title: The complete amino acid sequence of chitinase-a from the seeds of rye (Secale of A; Reference number: JC2071; MUID: 94169514
A; Reference number: JC2071
A; Reference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DYCGPRCQSQCTGCG-----GGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDA 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 PSYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 73.4%; Score 1315; DB 2; Local Similarity 76.1%; Pred. No. 1.8e-93; Les 229; Conservative 24; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRIGEYKRYCDIFGIGYGNNLDCYNQLSFN----VGLAAQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.0%; Score 1326.5; DB 70.9%; Pred. No. 2.6e-94; iive 29; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 74.0°
Best Local Similarity 70.9°
Matches 241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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**Rexperimental source: leaf, strain IRS8
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-32.Domain: signal sequence #status predicted <SIG>F;33-335/Froduct: chitinase #status predicted <AMAP>F;33-74/Domain: hevein chitin-binding domain homology <HCB>F;90-325/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable chitinase (EC 3.2.1.14) precursor - rice
C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 AAAGAFPAFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCDQSADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: U02286; NID: 9495302; PIDN: AAA18585.1; PID: 9495303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYCGPRCQSQCTGCG-----GGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFL 109
                                                                                                                                                                                                         245 SHDVITGRWSPSGADQAAGRVPCYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLG 304
                                                                                                                                                                                 72 G------GGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTT 121
                                                                                                                                                                                                                                                                             122 GDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 CHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFG 301
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                                           Gaps
                                                                                       VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSTLRARCATA----VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 GKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPS
                                                                                                                                   5 VVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGSTSDYCGNGCQSQCNGCSG
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                                           10;
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                                              49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
Score 1283; DB 2;
Pred. No. 5.2e-91;
                                                34; Mismatches
  71.6%;
70.5%;
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237; Conserv
                             Similarity
                                                Matches 222;
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Best Local Si
Matches 237;
       Query Match
                               Local
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R;Leah, R.; Skriver, K.; Knudsen, S.; Ruud-Hansen, J.; Raikhel, N.V.; Mundy, J.
Blant J. 6, 579-589, 1994
Briant J. 6, 579-589, 1994
Briant J. 6, 579-589, 1994
A;Title: Identification of an enhancer/silencer sequence directing the aleurone-specific A;Reference number: Z15373; MUID:95078949
A;Reference number: Z15373; MUID:95078949
A;Accession: T04484
A;Accession: T04484
A;Accession: T04484
A;Residues: J-332 <LEA>
A;Corser-references: EMBL:L34211; NID:9576566; PIDN:AAA56787.1; PID:9507961
C;Guperfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Superfamily: hevein chitin-binding domain homology <HCB>
F;28-69/Domain: plant chitinase homology <PCH>
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A)Cross-references: EMBL:X76041; NID:9416028; PIDN:CAA53626.1; PID:9416029
C)Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; C;Keywords: glycosidase; hydrolase; polysaccharide degradation
E)21-62/Domain: hevein chitin-binding domain homology <HCB>
F)21-62/Domain: plant chitinase homology <PCH>
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 22-Jun-1999
                                                                                                   C,Species: Hordeum vulgare (barley)
C,Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 APGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 PSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 PSSHAVITGQWTPTAADTAAGRVPGYGVITNIINGGLECGRGADSRVADRIGFYQRYCNI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 CG-----GGGGGVASIVSRDLFERFILHRN-"-DAACLARGFYTYDAFLAAAGAFPAFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AIVAIVLSAALAMAMVVRAQQCGSQAGGATCPNCLCCSRFGYCGSTSDYCGAGCQSQCSG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 TTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AVLAVVLAAAAVTP--ATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
71.8%; Score 1287.5; DB 2; Length 332;
Best Local Similarity 71.0%; Pred. No. 2.4e-91;
Matches 230; Conservative 35; Mismatches 44; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reisener,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S38670
R;Liao, Y.C.; Kreuzaler, F.; Tiburzy, R.; Reisener submitted to the EMBL Data Library, November 1993
A;Reference number: S38670
A;Accession: S38670
A;Status: preliminary
A;Molecule type: DNA
                                                                           probable chitinase (EC 3.2.1.14) - barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 LGVGYGGNLDCYNQRPFVEGLLIQ 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 FGIGYGNNLDCYNQLSFNVGLAAQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - wheat
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chitinase (EC 3.2.1.14) - rice
NyAlterrate names: class I endochitinase
C;Species: Oryza sativa (rice)
C;Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: S14948
E;Huang, J.K.; Nen, i., Sweqle, M.; Tran, H.C.; Thin, T.H.; Naylor, H.M.; Muthukrishn
Plant Mol. Biol. 16, 479-480, 1991
A;Reference number: S14948; MUID:91370895
A;Recession: S14948
A;Retars: preliminary
A;Molecule type: DNA
A;Recius: preliminary
A;Molecule type: DNA
A;Recius: Drainary
A
                                                                                                                                                         A;Residues: 1-336 <MOL>
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; C;Superfamily: lectin-related plant chitinase; polysaccharide degradation C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;22-63/Domain: hevein chitin-binding domain homology <HCB>
F;81-320/Domain: plant chitinase homology <PCH>
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C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain
C; Keywords: glycosladase; hydrolase; polysaccharide degradation
F:19-60/Domain: hevein chitin-binding domain homology <HCB>
F:79-316/Domain: plant chitinase homology <PCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GCGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAF 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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|SQCSRLRRRRPDASGGGGSGVASIVSRSLFDLMLLHRNDAACPASNFYTYDAFVAAASAF
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Pred. No. 4.9e-86;
1; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 1230; DB 2;
Pred. No. 6.2e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
number: S15997; MUID:91238706
: S15997
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70.1%; Pre
tive 31;
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Best Local Similarity
Matches 221; Conserv
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Les 218; Conserv
                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-336 <MOL>
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                                                            A; Accession:
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C;Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C;Accession: S1599; #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C;Accession: S1599; C:J.
Mol. Gen. Genet. 226, 289-296, 1991
A;Title: Isolation and characterization of a rice gene encoding a basic chitinase.
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                                                                                                                           297
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                                                        WFWMTTQSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADR
                                                                                             240 WFWMIPQGNKPSSHDVVIGRWAP-RRDVAAGRA-GYGVITNIVNGGLEGGDGPDDRVANR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N; Alternate names: endochitinase
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                                                                                                                                                                                                 A;Cross-references: EMBL:U02605; NID:9467819; PIDN:AAA18332.1; PID:9467820 C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; C;Reywords: glycosidase; hydrolase c;Reywords: glycosidase; hydrolase E:19-61,Domain: hevein chitin-binding domain homology <HCB> F;71-310/Domain: plant chitinase homology <PCH>
                                                                  of mRNAs encoding basic chitinase and 1,3-b
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R; Xu, Y.; Zhu, Q.; Panbangred, W.; Shirasu, K.; Lamb, C.
Plant Mol. Biol. 30, 387-401, 1996
A; Title: Regulation, expression and function of a new basic chitinase gene
A; Reference number: S65771; MUID:96189256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chitinase (EC 3.2.1.14) class I precursor - rice
C;Species: Oryza sativa (rice)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 GVASIVSRDLFERFLLHRNDAACLARG-FYTYDAFLAAAGAFPAFGTTGDLDTRKREVAA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 FFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 ATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCT~ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 ALVVVATAPAVVAVQP---EQCGSQARGALCPNCLCCSQYGWCGSTSAYCGSGCQSQCRR 61
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TILFSVILLSASARQCGSQAGGALCASGLCCSKFGWCGDTNDYCGPGNCQSQCPGGPGPSG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 VLAAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQCTGCGGGGG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 THNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 ARDSAAGRVPGYGVIINVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQ
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                                                                                                                                                                                                                                                                                                                                                                    Score 1193; DB 2; ... Pred. No. 4e-84; ... Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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; Pred. No. 4.8e
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      66.6%; Score 1193;
66.8%; Pred. No. 4e
:ive 42; Mismatche
                                                                                                                                       A,Status: preliminary, translation not shown
A,Molecule type: mRNA
A,Residues: 1-318 <BEE>
                                                      A; Title: Primary structure and expression A; Reference number: S43317; MUID:94154255 A; Accession: S65019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.5%;
67.2%;
C; Accession: S65019
R; Beerhues, L.; Kombrink, E.
Plant Mol. Biol. 24, 353-367, 1994
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Best Local Similarity 67.23
Matches 217; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -322 <XU2>
                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 205; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S65771
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-322 <XUZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 LSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSFGNGL 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ciptinase (EC 3.2.1.14) class I - garden pea
CiSpecies: Pisum sativum (garden pea)
CiSpecies: Disum sativum (garden pea)
CiSpecies: D-oct-1995 #sequence_revision 03-Nov-1995 #text_change 22-Jun-1999
CiSpecies: D-oct-1995 #sequence_revision 03-Nov-1995 #text_change 22-Jun-1999
CiSpecies: D-oct-1995 #sequence_revision 05 #text_change 22-Jun-1999
CiSpecies: D-oct-1995 #sequence_revision 05 #text_change 22-Jun-1999
R;Chang, M.M.: Horovitz, D.; Culley, D.; Hadwiger, L.A.
A;Title: Molecular cloning and characterization of a pea chitinase gene expressed in restances: nonber: S56694; MUID:95306779
A;Reference number: S56694; MUID:95306779
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <CRBL:137876; NID:9598346; PIDN:AAA75196.1; PID:9598347
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p]
C;Superfamily: hevein chitinase homology <CRCB>
F;71-308/Domain: plant chitinase homology <CRCB>
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C;Species: Solanum tuberosum (potato)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RCQSQCTGCGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGT 120
                                                      242
                                                                                                                                                                                                                                         242 HAVITGQWTPSADDQAAGRVPGYGETTNIINGGVECGHGADDKVADRIGFYKRYCDMLGV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                             LDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQE-QGSPPSYCDQSADWPCAPG 182
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                                                                                                                                                     HDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGI
                                                                                                                        KQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSC
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Best Local Similarity
Matches 211; Conserv
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T07838
chitinase (EC 3.2.1.14) - cucurbit
C; Species: Cucurbita sp. (cucurbit)
C; Date: 14-May-1999 #text_change 20-Jun-2000
C; Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 20-Jun-2000
C; Accession: T07838
R; Baaka, M.
Submitted to the EMBL Data Library, June 1998
A; Accession: T07838
A; Accession: T07838
A; Molecule type: many
A; Molecule type: many
A; Molecule type: many
A; Molecule type: many
A; Cross references: EMBL:AB015655; PIDN:BAA31131.1
C; Genetics:
A; Gene: chitpl
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C; Keywords: qlycosidase; hydrolase; polysaccharide degradation
C; Keywords: qlycosidase; hydrolase; polysaccharide degradation
F; 20-61/Pommain: hevein chitinase homology <PCH>
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                                                                                                                                                                                                                      239 PQSPRPSCHAVMIGQWIPNGNDQAAGRVPGYGYVINIINGGVECGHGADSRVADRIGFYK 298
                                                                                                                                  175 ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT 234
                                                                                                                                                                                                    235 TQSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 VVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQC----TGCG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 IVLAFAFVLGAAAEQCGRQANGALCPNRLCCSQFGWCGNTDEYCKNNCQSQCTPPSTGGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLW
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                                                                                     62 QLRRRRPDRPSGGGGSGVASIVSRSLFDQMLLHRNDAACPAKNLYTYDAFVAAANAFPTF
                                                                                                                                                       --GCGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAF
                                                                  -GSPPSYCDQS
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                                                                  GTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ--
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69.0%; Pred. No. 1e-83;
:ive 31; Mismatches
                                                                                                                                                                                                                                                                                           299 RYCDMLGVSYGANLDCYNQRPFN 321
                                                                                                                                                                                                                                                                      295 RYCDIFGIGYGNNLDCYNQLSFN 317
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hes 211;
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                                                                  119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
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chitinase (EC 3.2.1.14) chi9 precursor - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 10.5ep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: 537344; 538838; 525637
R;Danhash, N.; Wagemakers, C.A.M.; van Kan, J.A.L.; de Wit, P.J.G.M.
Plant Mol. Biol. 22, 1017-1029; 1993
A;Title: Molecular characterization of four chitinase cDNAs obtained from Cladosporiu A;Reference number: 537341; MUID: 94003061
A;Residues: 1-32 and A A;Residues: 1-32 and A;Resid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 GVASIVSRDLFERFLLHRNDAACLAR-GFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 VLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQCTGCGGGGG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 ARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 66.1%; Score 1185; DB 1; Best Local Similarity 66.1%; Pred. No. 1.6e-83; Matches 203; Conservative 41; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3, 2002, 18:32:12
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

3, 2002, 18:48:31 ; Search time 78.59 Seconds Мау

Run on:

(without alignments) 150.690 Million cell updates/sec

US-09-534-229C-2 Title: Perfect score:

1 MSTLRARCATAVLAVVLAAA......rgnnldcynqlsfnvglaaq 323

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

100059 segs, 36664827 residues Searched: Total number of hits satisfying chosen parameters:

DB sed length: 2000000000 Minimum DB seq length: 0 Maximum DB seq length: 20

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P11955 hordeum vul P25765 oryza sativ P24626 oryza sativ P24266 oryza sativ P21226 pisum sativ C05538 lyoopersico P24091 nicotiana t P62404 solanum tub P52405 solanum tub P52405 solanum tub P52405 solanum tub P19171 arabidopsis Q09023 brassica na P36979 gossypium h P19171 arabidopsis Q09023 brassica na P36979 picotiana t Q39785 gossypium h P51013 picotiana t Q39785 gossypium h P51013 picotiana t Q53978 gossypium h P51013 picotiana t P6579 populus tri Q0531 lyoopersico P2901 petunia hyb P17514 nicotiana t P17514 nicotiana t P17514 nicotiana t P17514 nicotiana t P17514 nicotiana t P17514 nicotiana t P17514 nicotiana t
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Length	3318 3318 3318 3318 3324 3324 3324 3324 3324 3324 3324 332
% Query Match	4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Score	1230 1230 1230 1196.5 1185 1184 1184 1174 1174 1174 1174 1174 1174
7.0	11084800 1111111111111111111111111111111

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AGI_URTDI	CHIP_BETVU	CHIB_MAIZE	CHIA_MAIZE	CHI4_BRANA	CHI4_PHAVU	CHIT_DIOJA	CHIC_POPTR	IAMY_COILA	WIN2_SOLTU	CHI4_ARAHY	CHIB_ARAHY
Н:	-1	1	H	Н	Н	Н	Н	Н	Н	Н	m
372	288	269	280	268	270	250	121	133	211	46	46
39.5	33.3	32.6	32.3	29.5	28.8	27.9	15.6	14.8	11.7	11.6	10.8
707.5	296	585	578	528.5	516	500.5	279.5	266	210.5	208	194
34	35	36	37	38	36	40	47	42	43	44	45

ALIGNMENTS

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                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae; Triticeae, Hordeum.
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 141-318 FROM N.A.
SIRATN=CV. HIMALAXIA.
SYMPALM HIMALAXIA.
"Identification of an endochitinase cDNA clone from barley aleurone
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLANT MO. BIOL. 12:403-412(1989).

-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

-!- INDUCTION: BY ETHYLENE.

-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIR-CV. NK 1558; TISSUE-Leaf;
Ignatius S.M.J., Huang J., Muthukrishnan S.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                   01-0cr-1989 (Rel. 12, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
26 KDB ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14).
Hordeum vulgare (Barley).
                                   318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U02287; AAA18586.1; -...
EMBL; X15349; CAA33407.1; -...
PIR; S04131; S04131.
HSSP; P23951; 2BAA.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00182; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19.
ProDom; PR00451; CHITINBINDNG.
ProDom; PD000554; Glyco_hydro_19; 1.
ProDom; PD00059; Chitin_bind; 1.
SMART; SM00270; Chitbli, 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
                                     STANDARD;
                                                                                                                                                                                                                          NCBI_TaxID=4513;
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                                 CHI1_HORVU
P11955;
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                   CHI1_HORVU
RESULT
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CHAIN
DOMAIN
DISULFID
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                                                                                                                                                                                                                                                                                                   63 GSTPVTPIPSGGGGVSIVSRALFDRMLHRNDGACQAKGFYIYDAFVAAASAFRGFGTT 122
                                                                                                                                                                                                                                                                                      122 GDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAP 181
                                                                                                                                                                                                                                                                                                                                                                                                     243 SHAVITGOWSPSGTDRAAGRVPGFGVITNIVNGGIECGHGQDSRVADRIGFYKRYCDILG 302
                                                                                                                                                                                                                                          -------GGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTT 121
                                                                                                                                                                        Gaps
                                                                                                                                                                                              12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG 71
                                                                                                                                                                                                          CHITINASE_19_2; 1. idase; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLOCOSAMINE POLYMERS OF CHITIN.
SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
Mkaryota, Viridplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                               242 CHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFG
                                                                                                                                                                                                                                                                                                                                   182 GKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Gen. Genet. 226:289-296(1991).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=91238706; PubMed=2034221;
Zhu Q., Lamb C.J.;
"Isolation and characterization of a rice gene encoding a basic
                                                                                                                                                                        12;
                                POTENTIAL.
26 KDA BENDCCHITINASE 1.
CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                 72.4%; Score 1297; DB 1; Length 318; 74.0%; Pred. No. 3.2e-92;
                                                                                                                                                                        43; Indels
                                                                 3X SIMILARITY.
3Y SIMILARITY.
3Y SIMILARITY.
3Y SIMILARITY.
42D62B2FE8041954 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
BASIC ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14)
                                                                                                                                                                       27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONTAINING FUNGAL PATHOGENS.
                               Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            302 IGYGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                           303 VGYGNNLDCYSQRPF 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
            Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S15997; S15997.
HSSP; P23951; 2BAA.
                                            20
20
22
31
36
53
318 AA;
                                                                                                                                                              Similarity
 PROSITE; PS00774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4530;
                      Multigene family signat
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ID CHIZ_ORYSA
AC P25765;
            Hydrolase;
                                                      DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                 Query Match
                                                                                                                                                            Best Local
                                             CHAIN
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238 PQSPKPSCNAVATGQWTPSADDQRAGRVPGYGVITNIINGGLECGHGEDDRIADRIGFYK 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 PAFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 PGFAAAGDADTNKREVAAFLAQTSHETTGGWATAPDGPYTWGYCFKEENGGAGFDYCQQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 TQSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 IRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
BASIC ENDOCHITMASE I PRECURSOR (EC 3.2.1.14).
0xrza sativa (Rice).
ENERATORIA (Rice).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CV. JAPONICA; TISSUE=Seedling;
MEDLINE=91370895; PubMed=1893114;
Huang J.K., Wen L., Sweede M., Tran H.C., Thin T.H., Naylor H.M.,
Muthukrishnan S., Reeck G.R.,
"Nucleotide sequence of a rice genomic clone that encodes a class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASIC ENDOCHIINASE 2.
CHIIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; 7F4EC12650EA84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.6%; Score 1230; DB 1; Length 336; 69.3%; Pred. No. 4.4e-87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Mismatches
InterPro; IPR001002; Chitin_bind.
InterPro; IPR00726; Glyco_hydro_19.
Pfam, PP00182; chitin_binding; 1.
Pfam; PP00182; Glyco_hydro_19.
PRINTS; PR00421; CHTTINBIRDNG.
PRODOM; PD000574; Glyco_hydro_19; 1.
PRODOM; P0000609; Chitin_bind; 1.
SMART; SM00270; ChtBD1; 1.
PROSITE; PS00773; CHTIN_BINDING; 1.
PROSITE; PS00773; CHTINASE 19.1; 1.
PROSITE; PS00774; CHTINASE 19.1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 RYCDIFGIGYGNNLDCYNQ 313
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Glycos
Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBL_TaxID=4530;
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P24626;
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        RESULT
CHI2_PEA
                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R PIR; S14948; S14948.

R INCEPPO: 1PR001002; Chitin_bind.
R InterPro: 1PR0010726; Glyco_hydro_19.
R Prem: PF00182; Glyco_hydro_19.
R Prem: PF00182; Glyco_hydro_19; 1.
R PRODOM: PD000609; Chitin_bind; 1.
R ProDom: PD000674; Glyco_hydro_19; 1.
R PRODOM: PD000609; Chitin_bind; 1.
R PROSITE: PS00026; CHITIN_BINDING; 1.
R PROSITE: PS000773; CHITIN_BINDING; 1.
R PROSITE: PS00774; PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GPTPPSSGGSGVASIISPSLFDQMLLHRNDQACRAKGFYTXDAFVAAANAYPDFATTRD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 LDTRKREVAAFFGQISHETIGGWPIAPDGPFSWGYCFKQE-QGSPPSYCDQSADWPCAPG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 HDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 -----GGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LALAVVAMAVVAVRGEQCGSQAGGALCPNCLCCSQYGWCGSTSDYCGAGCQSQCSGGCGG 63
                                                                                                            CATALTTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
SIMILARITY: BELONGS TO CHITINNES CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALTIC PRAT BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 KQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSC
Plant Mol. Biol. 16:479-480(1991).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
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CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
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: SIMILARITY.
8FD37913450CC7EB CRC64;
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318 AA;
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Multigene 1
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                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                       STRAIN=CV. ALCAN,
MEDLINE=95306779; PubMed=7787175;
Chang M.M., Horovitz D., Culley D., Hadwiger L.A.;
"Molecular cloning and characterization of a pea chitinase gene expressed in response to wounding, fungal infection and the elicitor chitosan.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REMOVED IN MATURE FORM (BY SIMILARITY). CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. BIRTE; TISSUE-Leaf;
Vad K., Mikkelsen J.D., Collinge D.B.;
"Induction, purification and characterization of chitinase isolated
"Induction, purification and characterization of chitinase isolated
"Induction, purification and characterization of chitinase isolated
Firom pea leaves inoculated with Ascochyta pisi.";
Planta 184:24-29(1991).
-1- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARIY: FIELD NGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
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InterPro; IPR001025; Glyco_hydro_19.
Ffam; PF00187; chitin_binding; 1.
Ffam; PF00187; chitin_binding; 1.
Ffam; PF00187; chitin_binding; 1.
Fromp, PF000187; Glyco_hydro_19; 1.
FRINTS; PR00451; CHITINBINDNG;
FROMP; SM00270; CHEBD; 1.
FROSITE; PS00773; CHITINSE_19_1; 1.
FROSITE; PS00773; CHITINSE_19_2; 1.
FROSITE; PS00774; CHITINSE_19_2; 1.
FROSITE; PS00774; CHITINSE_19_2; 1.
FROSITE; PS00774; CHITINSE_19_2; 1.
FROSITE; PS00774; CHITINSE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONTAINING FUNGAL PATHOGENS.
-!-CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- INDUCTION: FOLLOWING INFECTION WITH THE FUNGAL PATHOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
SIMILARITY.
540F0DA5EC1DC2FA CRC64;
                                 01-MAY-1991 (Rel. 18, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
115-1JUL-1999 (Rel. 38, Last annotation update)
ENDOCHITINASE A2 PRECURSOR (EC 3.2.1.14).
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BY SIMILARITY.
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 PRT;
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62
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34678 M
                                                                                                                             Pisum sativum (Garden pea).
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SIGNAL 1 20
 STANDARD;
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                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 21-36.
                                                                                                                                                                                                      NCBI_TaxID=3888;
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CHI2_PEA
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or send an email to license@isb-sib.ch)
                                                                       P23951;
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DISULFID
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: HYDROLYGIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
-!- DEVELOPMENTAL STAGE: HIGHEST LEAVES IN YOUNGER LEAVES OR STEMS SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TO INFECTION, ELICITOR, ETHYLENE, WOUNDING
                                                                                                                                                                                                               61 RCQSQCTGCGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGT 120
                                                                                                                                                                                                                                             IGDLDTRKREVAAFFGQTSHETIGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCA 180
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                1 MSTLRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. DATURA; TISSUE=Leaf;
MEDLINE=94154255; bubmed=8111037;
MEDLINE=94154255; bubmed=811037;
MEDLINE=94154255; bubmed=811037;
MEDLINE=94154255; bubmed=811037;
MEDLINE=941542545; bubmed=811037;
MEDLINE=11037;
MEDLINE=11037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Solanum tuberosum (Potato).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; eusterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                      1 MSKLR------IPILLVLFIVSCCSAEQCGTQAGGALCPGGLCCSKFGWCGSTSEYCGD
                                                                                                                                                                                                                                                                                                                                                                                                                                     PGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHDVITGLWTPTARDSAAGRVPGYGVITHVINGGIECGMGQNDKVADRIGFYKRYCDIF
                                                                     6
                    Length 324;
                                                                     58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
                    DB 1;
                 66.8%; Score 1196.5; DB 65.9%; Pred. No. 1.5e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 AA.
                                                                  42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OLD ROOT SEGMENTS, AND CARPELS. INDUCTION: IN RESPONSE TO INFEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 GIGYGNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 GIGYGDNLDCYSQRPFGSSL 311
                                           Best Local Similarity 65.9 Matches 211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asteridae; euast
NCBI_TaxID=4113;
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P52403;
                    Query Match
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CHIL_SOLTU
                                                                                                                                                                                                                                                                                                                121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 ARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 FFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 VLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQCTGCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TARGETING (POTENTIAL).
CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A0B49DA528706AAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHIC_LYCES STANDARD, PRT, 322 AA. 005538; 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 01-OCT-1994 (Rel. 30, Last annotation update) BASIC 30 KDA ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.6%; Score 1193; DB 1;
66.8%; Pred. No. 2.8e-84;
live 42; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
ENDOCHITINASE 1.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                       InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pr001000; PF00182; Glyco_hydro_19; 1.
Pr0Dom; PD000659; Chitin_bind; 1.
SWART; SW00270; Chitin_bind; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00778; CHITINASE_19_1; 1.
PROSITE; PS00778; CHITINASE_19_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
36
42
BY
49
58
33813 MW;
U02605; AAA18332.1;
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18
311
318
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es 205; Conserv
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Multigene family.
NON_TER 1
SIGNAL <1
CHAIN 19
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21
30
35
54
318 /
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DT 01-0708
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CHI2_TOBAC
P24091;
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                                                                                                                                                                                     RESULT 7
CHI2_TOBAC
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                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 FFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 THNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLFSVLLLSASAEQCGSQAGGALCASGLCCSKFGWCGNTNEYCGPGNCQSQCPGGPGPSG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS, PRO0451, CHITLMINDM.
PRODOM: PRO0609; CHITLMINDM.
ProDOM: PD0000609; Chitin_bind; 1.
ProDOM: PE0000609; Chitin_bind; 1.
PROSTTE; PS00026; CHITIN_BINDING; 1.
PROSTTE; PS00773; CHITINASE_19_1; 1.
PROSTE; PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                 -1- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 VLAAAAVIPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQCTGCGGGGG
                                             Danhash N., Wagemakers C.A.M., Van Kan J.A.L., de Wit P.J.G.M.;
"Molecular characterization of four chitinase cDNAs obtained from Cladosporium fullyum-infected tomato.";
Plant Mol. Biol. 22:1017-1029(1993).
-1- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REMOVED IN MATURE FORM.
CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASIC 30 KDA ENDOCHITINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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Pred. No. 1.2e-83;
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BY SIMILARITY
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-CV. MONEYMAKER;
MEDLINE-94003061; PubMed=8400122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001002; Chitin bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydroxylation; Multigene family. SIGNAL 1 22
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M
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66.18;
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PIR; S37344; S37344.
HSSP; P23951; 2BAA.
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                                                                                                                                                                                                                                                                    HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203;
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MOD_RES
SEQUENCE
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PROPEP
DOMAIN
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Shinshi H., Mohnen D., Meins F. Jr.; "Regulation of a plant pathogenesis-related enzyme: inhibition of chitinase and chitinase mRNA accumulation in cultured tobacco tissues
                                                                                                      191 SHNYNYGPCGRAIGVDLLNNPDLVATDPVISFKSAIWFWMTPQSPKPSCHDVITGRWQPS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
-!- INDUCATION: BY ETHYLENE.
-!- SIMILARIY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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                                                                       254 ARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fukuda Y., Ohme M., Shinshi H.;
"Gene structure and expression of a tobacco endochitinase gene in suspension-cultured tobacco cells.";
Plant MO1. Biol. 16:1-10(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92052270; pubMed=1946457; Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.; Sticher L., Meins F. Jr., Boller T.; As short C-terminal sequence is necessary and sufficient for the targeting of chitinases to the plant vacuole."; Proc. Natl. Acad. Sci. U.S.A. 88:10362-10366(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sticher I., Hofsteenge J., Milani A., Neuhaus J.M., Meins F. Jr.; "Vacuolar chitinases of tobacco: a new class of hydroxyproline-containing proteins."; Science 257:655-657(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF
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SEQUENCE OF 15-324 FROM N.A., AND SEQUENCE OF 24-53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-C7T-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE B PRECURSOR (EC 3.2.1.14) (CHN-B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 AA
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STRAIN-CV. BRIGHT YELLOW 4; TISSUE-Leaf;
MEDLINE-91363829; PubMed=1883889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CV. HAVANA 425; TISSUE-Leaf;
MEDLINE-92269767; PubMed=1588915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana tabacum (Common tobacco)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                               314 LSFNVGL 320
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HYDROXYLATION.
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                                                                                                                                                                                                                                                                                                         PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00743; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
PHOROLES; Glycosidase; Chitin degradation; Chitin-binding; Signal; Hydrolase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                    REMOVED IN MATURE FORM (PROBABLE)
CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.1%; Score 1184; DB 1; Length 324; 64.7%; Pred. No. 1.4e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63; Indels
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FA65DC2113B33EB6 CRC64;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
HYDROXYLATION.
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                                                                                                                                                                                                    InterPro; IPR001002; Chitin_bind.
InterPro; IPR00126; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000659; Chitin_bind; 1.
PRODOM; PD000669; Chitin_bind; 1.
                                                                                                             EMBL; X51599; CAA35945.1; --
EMBL; X64519; CAA45822.1; --
EMBL; M15773; AAA34070.1; --
PIR; A29074; A29074.
PIR; S13322.
PIR; S20981; S20981.
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121 TGDLDTRKREVAAFFGGTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCA 180
                                                                                                                                        120 SGDTTARKREIAAFFAQTSHETTGGWATAPDGPYAWGYCWLREQGSPGDYCTPSGQWPCA 179
                                                                                                                                                                             240
                                                                                                                                                                                      241 SCHDVITGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIF 300
                                                       63 QSQCTG--CGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGT 120
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ENDOCHITINASE A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. HAVANA 425, IISSUE-Leaf,
MEDLINE-91346623; PubMed=1966383;
Shinshi H., Neuhaus J.-M., Ryals J., Meins F. Jr.;
"Structure of a tobacco endochitinase gene: evidence that different chitinase genes an arise by transposition of sequences encoding a cysteine-rich domain.";
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Probom; PD000609; Chitin_bind; 1.
SWART; SW00270; ChITIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                    Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

NCBL_TaxID=4097;
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-1- CATALTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GIJCCOSAMINERS OF CHITIN.
-1- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
-1- NUDCTION: BY ENHYLENE.
-1- STHALLARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITINASE LIBRALIARITY: BELONGS TO CHITINASE CLASS IS N-TERMINAL CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITINASE LIBRALIARIES OF CHITINASE CLASS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92052270; PubMed-1946457;
Neukaus J.M., Sticher L., Meins F. Jr., Boller T.;
A short C-terminal sequence is necessary and sufficient for the targeting of chitinases to the plant vacuole.";
Proc. Natl. Acad. Sci. U.S.A. 88:10362-10366(1991).
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Sticher L., Hofsteenge J., Milani A., Neuhaus J.M., Meins F. Jr
"Vacuolar chitinases of tobacco: a new class of hydroxyproline-
                                                                                                  01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE A PRECURSOR (EC 3.2.1.14) (CHN-A).
       329 AA.
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HSSP; P23951; 2BAA.
InterPro; IPR001002; Chitin_bind.
Interpro; IPR001005; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Mol. Biol. 14:357-368(1990).
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                                                                 01-AUG-1988 (Rel. 08, Created)
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Science 257:655-657(1992),
       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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CHII_TOBAC
P08252;
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HARE REPRESENTED TO THE REPRESENTATION OF THE PROPERTY OF THE
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SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
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33798 ]
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318 AA;
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                                                                                                                                                                                                                                              64 PGGPTPTPPTPPGGGDLGSISSSMFDQMLKHRNDNACQGKGFYSYNAFINAARSFPGFG 123
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                                                                                                                                                                                                                                                                                                                                                         240 PSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYRRYCDI 299
                                                                                                                                                                                                                                                                                                                                                                     and 1,3-beta-glucanase in potato...,
Plant Mol. Biol. 24:353-367(1994).

-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POITWERS OF CHITIN.

-!- SUBCELLULAR LOCATION: VACOULAR AND PROTOPLAST (BY SIMILARITY).

-!- DEVELOPMENTAL STRAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS
SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE
                                                                                                                                                                           Gaps
                                                                                                                                                                                              99
                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beerhues L., Kombrink E.; "Primary structure and expression of mRNAs encoding basic chitinase
                                                                                                                                                                                                        180 APGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Solanum tuberosum (Potato).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                          8 CATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDXCGP-RCQSQC
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ω
        CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                       Length 329;
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                                                                                                             HYDROXYLATION (PARTIAL).
3EC99D96E6C0114C CRC64:
                                                          HYDROXYLATION (PARTIAL) HYDROXYLATION.
  REMOVED IN MATURE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-007-1996 (Rel. 34, Created)
01-007-1996 (Rel. 34, Last sequence update)
01-007-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 3 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
                                                                                                                                                    Score 1181; DB 1;
Pred. No. 2.4e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 AA
                                                                               HYDROXYLATION
                                                                                         HYDROXYLATION.
                                                                                                    HYDROXYLATION
                                                                                                                                                                        44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV. DATURA; TISSUE-Leaf;
MEDLINE-94154255; PubMed-8111037;
                                                                                                                                                                                                                                                                                                                                                                                                  300 FGIGYGNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                              304 LGVSPGDNLDCGNQRSFGNGL 324
                                                                                                                       MW.
                                                                                                                                                     65.9%;
63.6%;
329
655
441
653
663
667
771
772
35156
                                                                                                                                                             Best Local Similarity 63.6
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                     329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                        40
59
69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4113;
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P52405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
OLD ROOT SEGMENTS, AND CARPELS.
-!- INDUCTION: IN RESPONSE TO INTECTION, ELICITOR, ETHYLENE, WOUNDING.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLIDE A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 LFERFLLHRNDAACLAR-GFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFFGQTSHET 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 MFDQMLNHRNDNACQGKNNFYSYNAFISAAGSFPGFGTTGDITARKREIAAFLAQTSHET 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSAAGRV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 IGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGPA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 ATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQCTGCGGGGGGVASIVSRD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 ASAEQCGSQAGGALCAPGLCCSKFGWCGNTNDYCGPGNCQSQCPGGPGGPSGDLGGVISNS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
ProDom; PD0006574; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
ProSITE; PS00026; Chitin_bind; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 PGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TARGETING (POTENTIAL).
CHTIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; BF587A8515534E71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENDOCHITINASE 3. REMOVED IN MATURE FORM, VACUOLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.7%; Score 1177; DB 1; 67.4%; Pred. No. 4.7e-83; tive 40; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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7 LLFSVLLLSASAEQCGSQAGGALCASGLCCSKFGWCGNTNDYCGPGNCQSQCP--GGSPG 64 GVASIVSRDLFERFLLHRNDAACLARG-FYTYDAFLAAAGAFPAFGTTGDLDTRKREVAA

321 AA

PRT;

STANDARD;

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SEQUENCE FROM N.A.
Snyder-Leiby T.E., Furtek D.B.;
"A genomic clone from Theobroma cacao L. with high similarity to plant
                                                                                                          134 FFGQISHETIGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theobroma cacao (Cacao) (Cocoa).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Theobroma.
                                                                                                                                                                                                                  194 THNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPT
                                                                                                                                                                                                                                                                                                                                                                                               254 ARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQ
                                                                                                                                                                                                                                                                                                                                                                                                                              class I endochitinase sequences.";
(In) Plant Gene Register PGR95-056.
-!- FUNCTION: THIS PROPEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last Sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 LSFNVGL 320
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Q41596;
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                                                                                                                                                                                                                                                                               RC STRAIN-CV. DATURA: TISSUE=leaf;

RX MEDLINE=94154255, PubMed=8111037;

REDLINE=94154255, PubMed=811037;

REDLINE=94154255, PubMed=811037;

REDLINE=94154255, PubMed=811037;

REDLINE ROTORINE PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN

CONTAINING FUNGAL PATHOGENS.

CONTAINING FUNGATION: ACCOUNTER.

CONTAINING FUNGATION APPRECIABLE AMOUNTS ARE ALSO FOUND IN COLD ROOT SEGMENTS. AND CARPELS.

COLD ROOT SEGMENTS.

COLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                       Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWART; SM00270; ChtBbl; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITINASE 19_1; 1.
PROSITE; PS00774; CHITINASE 19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REMOVED IN MATURE FORM, VACUOLAR
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CHITIN BINDING (BY SIM)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENDOCHITINASE 2.
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InterPro; IPR001002; Glyco_hydro_19.
Pfan, PF00187; chitin_binding; 1.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000699; Glyco_hydro_19; 1.
ProDom; PD0006099; Ghyco_hydro_19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
36
42
BB 49
58
33629 MW;
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309
316
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21
30
35
54
316 AA;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                        Asteridae; euaste
NCBI_TaxID=4113;
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310
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SIGNAL
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-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SUBJULAR LOCATION: VACUOLAR AND PROMOPLAST (BY SIMILARITY).
-!- INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
-!- SIMILARITY: BELONGS TO CHITINSEE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT.WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Sont send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00182; Glyco_hydro_19; I.
PRNYS; PR00451; CHTINBIDNG.
ProDom; PD000574; Glyco_hydro_19; I.
ProDom; PD000609; Chitin_bind; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U30324; AAA80656.1; -.
HSSF; P02877; 1HEV.
Mendel; 1622; Thecc;Chial;1622.
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                                                                                                                                                                                                                                                                                                                      HYDROLASES)
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Gaps

4;

65.5%; Score 1174; DB 1; Length 316; 66.1%; Pred. No. 7.8e-83; -ive 42; Mismatches 58; Indels

Conservative

Local Similarity

Query Match

203;

Matches

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4
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                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ENDOCHTINASE I PRECOUSOR (EC 3.2.1.14).
GOSSYPALUM hirsutum (Upland coctton).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                         84 LFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFFGGTSHETT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                    144 G--GWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPLQLTHNYNYGP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 AGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSAAGR 261
                                                                                                                                                                                                                                                                                                               26 TAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPR--CQSQCTGCGGGGGGGVASIVSRD 83
                                                                                                                                                                                                                                                                                                                                      20 SARQCGRQAGGALCPGGLCCSQFGWGNTDDYCKKENGCQSQCSGSGGDTGGLDSLITRE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 VPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLSFNVG 319
PS00026; CHTIN_BINDING; 1.
PS00773; CHTINASE_19_1; 1.
PS00774; CHTINASE_19_2; 1.
e; Glycosidase; Chitin degradation; Chitin-binding; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. COKER 201;
Levorson J.v., Chlan C.A.;
Lisotation of a genomic DNA clone from Gossypium hirsutum with high
similarity to class I endochitinase plant sequences.";
(In) Plant Gene Register PGR96-054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- FUNCTION: DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
-1- FUNCTION: DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
-1- GALIYITC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLOOSAMINE POLYMERS OF CHITIN.
-1- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                          ,
9
                                                                                                                                                                                                                                                    65.1%; Score 1166; DB 1; Length 321;
69.1%; Pred. No. 3.2e-82;
Live 33; Mismatches 53; Indels
                                                                              ENDOCHITINASE 1.
CHITIN-BINDING (BY SIMILARITY)
                                                                                                           HINGE.
CATALYTIC.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
WY EBYDEBGSB7A2ADB CRC64;
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                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                        34847 MW;
                                                                                                                                                                                                                                                                 Best_Local Similarity 69.1%
Matches 206; Conservative
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                                                                 321
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SEQUENCE FROM N.A.
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                                                Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHI1_GOSHI
Q39799;
                                                                                                                                                                       DISULFID
DISULFID
SEQUENCE
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Best Local 8
 PROSITE;
                                PROSITE;
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                PROSITE;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 KREVAAFFGQISHETIG--GWPTAPDGFFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCG-PRCQSQCTGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                  Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 YGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 ITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          62; Indels
                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
9923B123EFSC7E3E CRC64;
                                                                                                                                                                                                                                                                           ENDOCHITINASE 1.
REMOVED IN MATURE FORM (BY
                                                                                                                                                                                                                                                                                                                                                                                                          64.9%; Score 1163; DB 1;
65.5%; Pred. No. 5.5e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) BASIC ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Mismatches
modified and this statement is not remove
entities requires a license agreement (so
or send an email to license@isb-sib.ch).
                                                                             InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Glyco_hydro_19.
Pfam, PF00182; chitin_binding; 1.
Pfam, PF00182; Glyco_hydro_19.
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000544; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
SWART; SM00270; ChtBbl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                        PROSITE; PS00026; CHTTIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
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34666 MW;
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01-FEB-1991 (Rel. 17, Last seq
15-JUL-1998 (Rel. 36, Last anno
                                                       EMBL; U60197; AAB67842.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 65.59
Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNLDCYNQSPEGNGVS 320
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                                                                                                                                                                                                                                  Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                    324 AA;
                                                                                                                                                                                                                                               Multigene family
SIGNAL
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                                                                                                                                                                                                                                   Hydrolase;
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TRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQY

126

Q q $\delta \Delta$ g δŏ g δ qq

246 IIGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYG

YGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDV

305 NNLDCYNQLSFNVGL 320 GNLDCYNQRSFVNGL 317

303

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                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA.
STRAIN-CV. COLUMBIA.
Kaneko T., Katch T., Satc S., Nakamura A., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC
                                                                                                                                                                                                                                                                                                                   N-ACETYL-D-GLOCOSAMINE POLYMERS OF CHITIN.
SUBGELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
IISSUE SPECIFICITY: HIGH CONSTITUTIVE LEVEL. IN ROOTS WITH LOWER LEVELS IN LEAVES AND PROTOPLASTS.
IISSUE SPECIFICITY: HIGH CONSTITUTIVE LEVEL. IN ROOTS WITH LOWER LEVELS IN LEAVES AND PLOWERING SHOOTS.
INDUCTION: ETHYLENE INDUCES HIGH LEVELS OF SYSTEMIC EXPRESSION OF BASIC CHITINASE WITH EXPRESSION INCREASING WITH PLANT AGE.
SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL HYDROLASES).
HYDROLASES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal.
                                                                                                                                                                                                                                                RES. 7:217-221(2000).
FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
                                               Samac D.A., Hironaka C.M., Yallaly P.E., Shah D.M.;
"Isolation and characterization of the genes encoding basic and acidic chitinase in Arabidopsis thaliana.";
Plant Physiol. 93:907-914(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASIC ENDOCHITINASE.
REMOVED IN MATURE FORM (PROBABL.
CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C9AFFE4C544FCCD7 CRC64;
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ProDom; PD000609; Chitin_bind; 1.
SWART; SM00270; ChtBB1; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITINARE_19_1; 1.
PROSITE; PS00774; CHITINARE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001002; Chitin_bind.
InterPro; IPR007026; Glyco_hydro_19.
Pfam: PF00187; chitin_binding; 1.
Pfam: PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M38240; AAA32769.1; ALT_INIT.
EMBL; AP002047; BAB03157.1; -.
HSSP; P23951; 2BAA.
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315
522 F F 63
63 C C 38
44 B B B 51
51 B B 83
                 SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
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Eukaryota; Ŷiridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

01-0CT-1994 (Rel. 30, Created) 01-0CT-1994 (Rel. 30, Last sequence update) 01-0CT-1994 (Rel. 30, Last annotation update) ENDOCHITINASE CH25 PRECURSOR (EC 3.2.1.14).

01-0CT-1994 01-0CT-1994 CHI2_BRANA

00902

Brassica napus (Rape)

SEQUENCE FROM N.A. eurosids II, Bra NCBI_TaxID=3708;

322 AA

STANDARD;

RESULT 14 CHI2_BRANA

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                                                                                                                                                                                                                        MEDLINE-94143492; Pubmed=8310072; Hamel F., Bellemare G.; Allemare G.; Ballemare G.; Ballemare G.; Bellemare G.; Blant Physiol. 101:1403-1403(1993).

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLOCOSAMINE POLYMERS OF CHTIN.

-!- STMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHTIN BUT BELDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL)
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ENDOGHITINASE CH25.
CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRAWYS; PR00451; CHTTINBIENG
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000699; Chitin_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00026; CHITIN BINDING; 1. PS00773; CHITINASE_19_1; 1.
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HSSP; P23951; 2BAA.
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNLFLFLFFLFSLLLSLSSAEQCGRQAGGALCPNGLCCSEFGWCGNTEPYCKQPGCQSQCTP
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Pred. No. 2.7e-81;
1; Mismatches 69
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34;

Conservative

208;

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Similarity

Local

Best Loca Matches

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Query Match

64.48; 66.08;

DISULFID

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                                                                                                                                                                                                                                     69 C-GGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTR 127
                                                                                                                                                                                                                                                                                      187
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                              Gaps
                                                                                                                                                     10 TAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYC-GPRCQSQCTG 68
                                                                                                                                                                                             62
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SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                           SCELLFIFSFLSFSLAEQCGRQAGGALCPNGLCCSEFGWCGDFEAYCKQPGCQSGCG
                                                                                                                                                                                                                                                                              128 KREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. BIRTE; TISSUE-Leaf;
Vad K., de Neergaard E., Madriz-Ordenana K., Mikkelsen J.D.,
Collinge D.B.;
"Accumulation of defence-related transcripts and cloning of a
chitinase mRNA from pea leaves (Pisum sativum L.) inoculated with
Ascochyta pisi Lib.",
Plant Sci. 92:69-79(1993).
                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
                                                                                               Length 322;
                                                                                                                             Indels
 BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

E62EE4B17211DBCD CRC64;
                                                                                                                              68;
                                                                                          64.0%; Score 1146; DB 1;
66.3%; Pred. No. 1.1e-80;
11ve 34; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 AA
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44 B
51 B
60 B
34816 MW;
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
32
37
56
322 AA;
                                                                                         Query Match
Best Local Similarity
Matches 205; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 LDCYNQLSF 316
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DISULFID
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                             DISULFID
                                              SEQUENCE
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5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 SHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTHNYN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 YGPAGRAIGVDILNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSA 258
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 AEQCGSQAGGAVCPNGLCCSKFGFCGSTDPYCGDGCQSQCKSSPTPTIPTPSTGGGDVGR 82
                                                                                                                                 SMART; SM00270; ChtBDI; 1.
PROSITE; PS00026; CHTIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGRVPGYGVITHVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLSF 316
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6
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7PDEC8ClAECC3435 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                    27 AEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGC
                                                                                                                                                                                                                                                                                                                                  Score 1145.5; DB
Pred. No. 1.2e-80;
2; Mismatches 55
                                                                                                                                                                                                            BY SIMILARITY.
ENDOCHITINASE.
CHITIN-BINDING (
send an email to license@isb-sib.ch).
                                             InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Glyco_hydro_19.
Ffam; PF00187; chitin_binding; 1.
Ffam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3, 2002, 18:48:32
                                                                                                                                                                                                                                                                                                                                  63.9%; Sco.
67.8%; Pred
tive 32; 1
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320
64
41
47
54
54
62
B
                       EMBL; X63899; CAA45359.1;
HSSP; P02877; 1HEV.
                                                                                                                                                                                                                                                                                                                                                          Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                               Multigene family.
SIGNAL
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Job time: 916 sec
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DISULFID
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Мау Run on:

3, 2002, 18:46:59 ; Search time 157.87 Seconds (without alignments) 299.271 Million cell updates/sec

US-09-534-229C-2 Title:

Perfect score:

1792 1 MSTLRARCATAVLAVVLAAA......YGNNLDCYNQLSFNVGLAAQ 323 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 seqs, 146272329 residues Searched:

473505 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SPTREMBL_17:* Database

sp_archea:*
sp_bacteria:*
sp_fungi:* sp_human:*

sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_virus:*
sp_vertebrate:* sp_organelle:* sp_rodent:* sp_phage:* 5: 77: 70: 10: 110: 14: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

SUMMARIES

Description	Q9frv1 secale cere Q43294 oryza sativ Q9sq13 poa pratens Q4292 oryza sativ Q9axr9 secale cere Q42839 hordeum vul Q41539 triticum ae Q42940 oryza sativ Q42970 oryza sativ Q42970 oryza sativ Q42970 oryza sativ Q43970 oryza sativ Q38777 allium satil Q4295 oryza sativ Q38777 allium satil Q4295 oryza sativ Q38776 allium satil Q4295 oryza sativ Q80404 cucurbita m Q9fex1 nicotiana s Q9fex1 nicotiana s Q9fex1 nicotiana s	57.7
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& Query Match	44 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
Score	1326.5 1326.5 1310.5 1306.5 1204.5 1228.1 1272 1272 1272 1272 1273 1274 1192.4 1192.4 1192.4 1193.5 1185.5 1187.5 1187.5	
Result	10004000000000000000000000000000000000	

09m7q9 arabis glab 09m7q7 arabis glab P94084 medicago sa 09zpl0 cicer ariet 041180 nicotiana t 042428 castanea sa 09m7h0 arabis fecu 09sxj3 arabidopsis 09sxj3 arabidopsis 09sxj3 arabidopsis 09sxj4 arabidopsis 09m7f5 arabis pari 09m7f4 arabis pari 09m7f4 arabis pari 09m7f4 arabis germ 045887 arabidopsis 09sxj4 arabidopsis 09sxj4 arabidopsis 09sxj1 arabis germ 045887 vigna ungui 09m7h2 arabis germ	arabidcarabidcarabis arabis arabis arabis arabis
Q9M7G9 Q9M7G7 Q9ZPU0 Q9ZPU0 Q411B0 Q42428 Q942428 Q94746 Q987J5 Q987J5 Q987J6 Q9M7F5 Q9M7H2 Q436B5 Q947B5 Q947B5 Q947B2	Q9SXJ2 Q9M7G2 Q9M7G4 Q9M7G1 Q9M7F6
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33 30041 - 2000 30041 - 2000 3000 3000 3000 3000 3000 3000 3000	335 306 302 300 294 299
00000000000000000000000000000000000000	64.1 63.2 63.2 63.0 62.6
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01000000000000000000000000000000000000	4444 011 543 543

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Secale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 ATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGFRCQSQCTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Chnuma T. Yamaqami T., Ishiguro M.;
"Cloning and Sequencing of the Rye Seed Chitinase.";
Lyamatited (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB051578; BAB18519.1.
InterPro; IPR001002; Chitin.bind.
R InterPro; IPR001002; Chitin.bind.
R Pfam; PF00187; Chitin.binding; 1.
R Pfam; PF00187; Chitin.binding; 1.
R Pfam; PF00187; CHITINBINDNG.
R ProDom; PD000574; Glyco_hydro_19; 1.
R ProDom; PD000609; Chitin_bind; 1.
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                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.4%; Score 1334; DB 10;
74.4%; Pred. No. 2.2e-112;
tive 26; Mismatches 42;
                                                                                      321 AA.
                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00270; ChtBD1; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
                                                                                   PRT;
                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 74.43
Matches 238; Conservative
                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                         Secale cereale (Rye)
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                                                                                                                                                                                                                                                         SEED CHITINASE-A.
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SEQUENCE 321
                                                                                                         Q9FRV1;
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RESULT
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DYCGPRCQSQCTGCG-----GGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDA 107 |:|| |||||:||| |DFCGDGCQSQCSGCGPTPTPPSPSDGVGSIVPRDLFERLLLHRNDGACPARGFYTYBA 120

FLAAAGAFPAFGITGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEGGSP

DRIGETKRYCDIFGIGYGNNLDCYNQLSFN----VGLAAQ 323

167 180 227

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228 AIWFWMTTQSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVA 287
                                                                                                                                                                                                                                                                            168 PSYCDQSADWFCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNFDLVATDPTVAFKT
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117 AFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSAD 176
                                                                                                                                          236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-JAPONICA, CV. NIPPONBARE;
MEDLINE=94049667; PubMed-7901749;
Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
"Sequence variation, differential expression and chromosomal location
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1.4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                        WPCARGKQYYGRGPIQLTHNYNYGPAGRAIGYDLLNNPDLVATDPIVAFKTALWFWMTTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of the sequence o
                                                                                                                                                                                            SNKPSCHDVIIGLWTPIARDSAAGRVPGYGVIINVINGGIECGMGQNDKVADRIGFYKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   642F13E3928CA7BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.0%; Score 1326.5; DB 1(70.9%; Pred. No. 1.1e-111; tive 29; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycosidase; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                   340 AA
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                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                               297 CDIFGIGYGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                       35586 MW;
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01-NOV-1996 (TrEMBLrel.
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Poa pratensis (Kentucky bluegrass).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLDTRKREVAAFFGQTSHETIGGWPIAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 PTPVTPTPSGGGGVSSIVSQSLFEQMLLHRNDAACLAKGEYTYNAF1AANSFAGFGTTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF000966; ARF04454.1; ---
HSSP; P29351, 2BAA.

R InterPro: IPR001002; Chitin_bind.

R InterPro: IPR001002; Chitin_bind.

Pfam: PF00182; Glycc_hydro_19.

R Pfam: PF00182; Glycc_hydro_19; 1.

PRINTS; PR00451, CHITINIBIRDNG.

R ProDom: PD000609; Chitin_bind; 1.

PROSTIE: PS000774; Glycc_hydro_19; 1.

R PROSTIE: PS00774; CHITINISE_19.1;

R PROSTIE: PS00774; CHITINISE_19.2;

R PHOSTIE: PS000726; CHITINISE_19.2;

R PHOSTIE: PS000736; CHITIN
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                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.5%; Score 1317.5; DB 10; 72.6%; Pred. No. 6.7e-111; Live 33; Mismatches 44; In
320 AA
                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 13, C
(TrEMBLrel. 13, I
(TrEMBLrel. 17, I
                                                                                                                                                                                                                                   PRELIMINARY;
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Best Local Similarity
Matches 228; Conserv
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01-MAY-2000 (
01-JUN-2001 (
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53; Indels

Local Similarity 70.9

Best Loca Matches

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DB 10; Length 340;

1 MSTLRARCATA-----VLAVVLAAAAVTPATAEQCGSQAGGAKCADGLCCSQFGFCGTTS 55

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Local Similarity 71.6 ses 224; Conservative
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 YGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                   cereale (Rye).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 YGHNLDCYNQRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lajoie G.;
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Q42839;
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Matches
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183 KQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSC 242
                        (1,4-BETA-POLY-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 GGGGGG------VASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 GGGGGGGGGGGGGGGGAVEAVSKELFEQLLLHRNDAACPARGFYTYDAFVTAAAAFP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSAD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQ 236
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                                                                                  HDVITGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
Wkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 TAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTISDYCGPRCQSQCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN=IR36; TISSUE=ETIOLATED LEAF;
Yun C.H., Kim J.K., Park Y.H.;
Yun C.H., Kim J.Y., Park Y.H.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-!- CAPALYIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF EMBL; 137289; AAAS1377.1; -...
HSSP; P23951; 2BAA.
Mendel; 26; Orysa; Chial; 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.9%; Score 1306.5; DB 10; Length 333; 70.6%; Pred. No. 6.9e-110; Live 35; Mismatches 48; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E2B65D4155B8C73D CRC64;
                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINNSE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE)
ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycosidase; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                               333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mendel, 26; Orysa, Chial; 26.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001726; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
PRINTS; PR00451, CHITINBIADNG.
ProDom; PD000574; Glyco_hydro_19; 1.
SMARY, SM00270; Chitin_bind; 1.
PROSITE; PS00773; CHITINASE_19_1; PROSITE; PS00774; CHITINASE_19_2; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
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les 230; Conservative
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                      GYGNNLDCYNQLSF 316
                                                                                                                                                                                            305 SYGNNLDCYSQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chitin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                    243
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Wiseman S.B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 TPVPVPTPTGGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFIAAANSFSAFATTGG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 LDTRKREVAAFFGQISHETIGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 DVITGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIG 303
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VVVAMLAAABFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGSTSEYGGDGQSQCNRCGG 64
                                                         SNKPSCHDVITGIMIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 QYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Chitinase genes responsive to cold encode antifreeze proteins winter cereals.", Plant Physiol. 124:1251-1264(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 318;
                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
31.7 KDA CLASS I ENDOCHITINASE-ANTIFREEZE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20532799; Pubmed=11080301;
Yeh S., Moffatt B., Griffith M., Xiong F., Yang D.S.C., Wis
Sarhan F., Danyluk J., Xue Y.Q., Hew C.L., Doherty-Kirby A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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BA685E1DB7A58E63 CRC64;
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                                                                                                                                                                                                                                                                                             318 AA.
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                                                                                                                                     297 CDIFGIGYGNNLDCYNQLSFNVGLAA 322
                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                              20
33636 MW;
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SOUR BRANK B

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72 G------GGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum (Wheat).
Exkaryota, Viridiplantae; Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 SHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGFRCQSQCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGSTSDYCGNGCQSQCNGCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 GDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 GKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 CHDVITGLWTPTARDSAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYKRYCDIFG
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN—CV. CHINESE SPRING;
Liao Y.C., Kreuzaler F., Fischer R., Reisener H.J., Tibuzzy R.;
Plant Sci. 103:177—198(1994).
EMBL; X76041; CAA53626.1;
EMBL; X76041; CAA53626.1;
EMBL; X76041; CAA53626.1;
HSSP; P23951; ZBAA.
Mendel; 1465; Triae; Chial; 1463.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR00102; Chitin_bind.
Pfam; PF00187; chitin_binding. 1.
Pfam; PF00187; chitin_binding. 1.
Pfam; PF00187; CHIINBINDNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
ENDOCHITINASE.
F258D9DD8EF65E0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
3.2.1.14).
                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENDOCHITINASE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.6%; Score 1283; DB 10;
70.5%; Pred. No. 8.6e-108;
Live 34; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000574; Glyco_hydro_19; 1. ProDom; PD000609; Chitin_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00270; ChtBD1; 1,
PROSITE; PS00774; CHITINASE_19_2;
PROSITE; PS00026; CHITIN_BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33602 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLEEL 01, C)
01-NOV-1996 (TrEMBLEEL 01, Ls
01-JUN-2001 (TrEMBLEEL 17, Ls
ENDOCHTINASE PRECURSOR (EC 3
CHIAL OR CHT-3.
Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 VTYGDNLDCYNQRPF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 IGYGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chitin-binding; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN 21
SEQUENCE 320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                           Triticeae; Triti
NCBI_TaxID=4565;
                                                                                                                 CHIA1 OR CHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Sim
les 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q42994
Q42994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     042994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q\overline{Q}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 CG-----GGGGGVASIVSRDLFERFILHRN---DAACLARGFYTYDAFLAAAGAFPAFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 ITGDLDTRKREVAAFFGQISHEITGGWPIAPDGPFSWGYCFKQEQGSPPSYCDQSADWPC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 APGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 PSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE (FC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
CHIA1 OR CHI33.
HOGGHum vulgare (Barley).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Mornollophyta; Liliopsida; Poales; Poaceae; Pooldeae; Withtheae, Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 AVLAVVLAAAAVTP--ATAEQCGSQAGGAKCADCLCCSQFGFGGTTSDYCGPRCQSQCTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mundy J.

Mundy J.

Mundy J.

Mundy J.

Identification of an enhancer/sllencer sequence directing the
aleurone-specific expression of a barley chitinase gene.";

Plant J. 6:579-589(1994).

ACTIVIT: BRICOSAMINE POLYMERS OF THE 1,4-BETA-LINKAGES OF N-
ACTIVIT: BROYON-CAMINE POLYMERS OF CHITIN.

EMBL: 134211; AAA567897.1:

RSP: P29551; ZBAA.

Macdel, 1565; Morvu Chial; 1565.

InterPro: IPROUOTZ5: Glyco_hydro_19.

Pfam: PF00187; chitin_bind.

Pfam: PF00187; chitin_bind.

Pfam: PF00187; chitin_bind.

Probom; P0000574; Glyco_hydro_19; 1.

Probom; P000574; CHITINANDWO.

PROSTIE: PS00773; CHITINASE_19.1; UNKNOWN_1.

PROSTIE: PS00773; CHITINASE_19.2; 1.

PROSTIE: PS00773; CHITINASE_19.2; 1.

PROSTIE: PS00774; CHITINASE_19.2; 1.

PROSTIE: PS00774; CHITINASE_19.2; 1.

PROSTIE: PS00774; CHITINASE_19.2; 1.

PROSTIE: PS00773; CHITINASE_19.2; 1.

PROSTIE: PS00774; CHITINASE_19.2; 1.

PROSTIE: PS00773; CHITINASE_19.2; 1.

PROSTIE: PS00774; CHITINASE_19.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 332;
                                                                                                                                                                                                                                                                                                                                                         Leah R., Skriver K., Knudsen S., Ruud-Hansen J., Ralkhel N.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.8%; Score 1287.5; DB 10
71.0%; Pred. No. 3.5e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 FGIGYGNNLDCYNQLSFNVGLAAQ 323
                                                                                                                                                                                                                                                                                                                                   MEDLINE=95078949; PubMed=7987416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 LGVGYGGNLDCYNQRPFVEGLLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 71.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                TISSUE=SEED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q41539
Q41539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
Q41539
ID Q4
AC Q4
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Gaps

64

181 184 301 304

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56 DYCGPRCQSQCTGCG-----GGGGGVASIVSRDLFERFILHRNDAACLARGFYTYDAFL 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 YCDQSADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLYATDPTVAFKTAI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 WFWMTTQSNKPSCHDVITGLWTFTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADR 289
                                                                                                                                            STRAIN-RADS; TISOUS-LEAF;
Submitted (SEP-1993) to the EMBL/GenBank/DBBJ databases.

1. CATALLYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GUCOSAMINE POLYMERS OF CHITIN.

REMB: 002286; AAA18585.1;
REMB: 002286; AAA18585.1;
REME: 002286; CAAA18585.1;
RICHERPEO: IPROUNCAS, CHILIN, DAIG.

REME: 002286; CAAA18585.1;
REME: 002286; CAAA18585.1;
REME: 002286; CAAA1857.

RICHERPEO: IPROUNCAS; GLYCO_HYD.

REME: 002286; CAAA1858.1;
REME: 002286; CAAA1888.1;
REME: 002286; CAAA18886; CAAA1888.1;
REME: 002286; CAAA18886; CAAA18886; CAAA18886; CAAA18886; CAAA18886; CAAA18886; CAAA18886; CAAA18886; CAAA18886; CAAAA18886; CAAA18886; CAAAA18886; CAAAA18886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Persea.
NCBI_TaxID=3435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 WFWMTPQGNKPSSHDVVTGRWAP-RRDVAAGRA-GYGVITNIVNGGLRCGDGPDDRVANR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSTLRARCATA-----VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSTPRAAASLAKKAALVALAVLAAALATAACAEQCGAQAGGARCPNCLCCSRWGWCGSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 335;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHITINASE. 47C5FC04D29573C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.0%; Score 1272; DB 10; 70.1%; Pred. No. 8.9e-107; iive 27; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 IGFYKRYCDIFGIGYGNNLDCYNQLSFN----VGLAAQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35166 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Persea americana (Avocado).
                                                                                                  SEQUENCE FROM N.A.
STRAIN=IR58; TISSUE=LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 237; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                    NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHIAL OR CHIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P93680
P93680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
P93680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ωÿ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
        ä;
                                                                                                                                                                       MEDLINE-94049667; Pubmed=7901749;
Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
"Sequence variation, differential expression and chromosomal location of rice chithrase genes.";
Mol. Gen. Genet. 241:1-10(1993).
BMBL; D16223; BAA03751.1;
HSSP, P23951; ZBAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 GPTPPSSGGGSGVASIISPSLFDQMLLHRNDQACAAKGFYTYDAFVAAANAYPDFATTGD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 LDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQE-QGSPPSYCDQSADWPCAPG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 -----GGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LALAVVAMAVVAVRGEQCGSQAGGALCPNCLCCSQYGWCGSTSDYCGAGCQSQCSGGCG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCT-GCG- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 KQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.2%; Score 1276; DB 10; Length 320; 72.0%; Pred. No. 3.7e-107; ive 32; Mismatches 45; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probom, Proposed Probability Probom, Proposed Proposed Proposition Chieffelist Prostre: Proof73; CHITIMASE 19_1; 1.
PROSTIE; PS00774; CHITIMASE 19_2; 1.
PROSTIE; PS00776; CHITIM.BINDING; 1.
Chitin-binding; Glycosidase; Hydrolase; Signal.
SIGNAL 1 18 PROCHITIMASE.
19 320 ENDCHITIMASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-1091 (TrEMBLrel. 17, Last annotation update)
CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE)
ACETICGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 AA.
                                                                                                                                                                                                                                                                                                                                                       Mendel, 12921, Orysa, Chial, 1582.

InterPro; 1PR001002; Chitin bind.

InterPro; 1PR001002; Chitin bind.

Ffam; PF00187; Chitin binding; 1.

Ffam; PF00182; Glyco_hydro_19; 1.

PRINTS; PR00451; CHITINENDNG.

PRODOM; P0000544; Glyco_hydro_19; 1.

ProDom; P0000549; Chitin_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 72.0
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 SYGDNEDCYNQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 GYGNNLDCYNQ 313
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                  STRAIN=NIPPONBARE;
                                                                                  NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      042970
042970;
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Length 340; Indels 64

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SEQUENCE FROM N.A.
STRAIN-MIPPOHBARE,
MEDLINE-94049667; PubMed=7901749;
Mishizawa Y., Kishimoto N., Saito A., Hibi T.;
"Sequence variation, differential expression and chromosomal location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GGGGVASIVS3DLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 PTPVTPTPSGGGGGVSSLVSQSLFEQMLLHRNDPSCQANGFYTXKAFIAAANSFAGFGTTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 DLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 KOYYGRGPIQLIHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 HDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDK--VADRIGFYKRYCDIF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04.2993; 042996 (TEMBLRel. 01, Created)
01-NOV-1996 (TEMBLRel. 01, Last sequence update)
01-NOV-1996 (TEMBLRel. 01, Last sequence update)
01-NOV-1996 (TEMBLRel. 01, Last sequence update)
01-JUN-2001 (TEMBLRel. 17, Last annotation update)
01-JUN-2001 (TEMBLRel. 17, Last annotation update)
01-JUN-2001 (TEMBLRel. 17, Last sequence u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 VVAILVAAFAVS-AHAEQCGSQAGGATCPNCLCCSKFGFCGNTSDYCGTGCQSQCNGCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 AA; 36011 MW; 3613D7059A871E94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.0%; Score 1254; DB 10; 69.3%; Pred. No. 3.8e-105; iive 40; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 AA.
                            InterPro; IPR001002; Chitin_bind.
InterPro; IPR0010025; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
Pfam; PF00187; Chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
Propom; PR000574; Glyco_hydro_19; 1.
Propom; PD000609; Chitin_bind; 1.
PROSITE; PS00779; Chitin_bind; 1.
PROSITE; PS00773; CHTINASE_19_1; 1.
PROSITE; PS00774; CHTINASE_19_2; 1.
PROSITE; PS00774; CHTINASE_19_2; 1.
Chitin-binding; A, 36011 MW; 3613D705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of rice chitinase genes.";
Mol. Gen. Genet. 241:1-10(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 21-323 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nishizawa Y., Hibi T.;
Plant Sci. 76:211-218(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GIGYGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: ||:|||||||: |
GVSYGDNLDCYNESPF 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 219; Conserv
    HSSP; P23951; 2BAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBL_TaxID=4530;
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042993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 IQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLW 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 TPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae, Pooldeae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGFTSDYCGFRCQSQCTG-CG 70
                            Sowka S., Hsieh, L., Krebitz M., Akasawa A., Martin B., Starrett D., A Peterbauer C., Scheiner O., Breiteneder H.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
RMSL; Z78202; CA801591.1; -.
RMSL; Z78202; CA801591.1; -.
RMSL; PORST; HREV
R Mendel: 14766; Perae:Chial:14766.
R InterPro; IPR001002; Chitin_bind.
R InterPro; IPR001002; Chitin_bind.
R Pfam; PF00187; chitin_bind.
R Pfam; PF00187; chitin_binding; 1.
R RFM: PR00187; chitin_binding; 1.
R RFM: PR00187; chitin_binding; 1.
R RINS; PR00451; CHITINBINDG.
R Probom; P0000509; chitin_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 VAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·.
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EMBL; AF000964; AAF04453.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             643B20589E062E61 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.1%; Score 1256; DB 10;
69.8%; Pred. No. 2.4e-105;
tive 36; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodom; PD040505; chrbbl; 1.
PROSITE; PS00774; CHTTINASE_19_1; 1.
PROSITE; PS00774; CHTTINASE_19_2; 1.
PROSITE; PS00026; CHTTIN_BINDING; 1.
Chitin-binding; Glycosidase; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENDOCHITINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Mismatches
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STRAIN-CV. HASS, TISSUE-MESOCARP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAX-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 YNQLSFNVG---LAA 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 3
326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Du M., Ha S.B.;
Submitted (APR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-GLADE;
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Q9SQL4
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Matches 212;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                ------CGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAF 118
                                                                                                                                                                                                                                                                                                                                                                             62 SCGGGGPTPPSGGGGSGVASIVSRSLFDQMLLHRNDAACPAKNFYTYDAFVAAANAFPSF 121
                                                                                                                                                                                                                                                                                                                                                                                                                         119 GTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ----GSPPSYCDQS 174
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 TQSNKPSCHDVITGLWTPTARDSAAGRVFGYGVIINVINGGIECCMGQNDKVADRIGFYK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAVLAVVLAAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGFRCQSQCTG 68
                                                                                                                                                                                                                                                                                                                                 C -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

REMBL, DIGESL; BAAA03749.1; -.

REMBL, X56063; CAA39535.1; -.

R HSSP; P23951; ZBAA.

R Mendel; 14776; CAYSa; Chial; 14776.

R InterPro; IPR001002; Chialin_bind.

R InterPro; IPR001002; Chialin_bind.

R Ffam; PF00187; Chitin_binding; 1.

R Ffam; PF00182; GlyCo_hydro_19; 1.

R PRINTS; PR00451; CHITINBINDNC.

PRODOM; PD000659; Chitin_bind; 1.

R PRODOM; PD00069; Chitin_bind; 1.

R PROSITE; PS00073; CHITINASE.19.1; 1.

R PROSITE; PS00073; CHITINASE.19.2; 1.

R PROSITE; PS00073; CHITINASE.19.2; 1.

R PROSITE; PS00074; CHITINASE.19.2; 1.

R Chitin_binding; GlyCosidase; Hydrolas.; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allium sativum (Sarlic).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Asparagales, Alliaceae,
Allium.
                                                                                                                                                                                                                                                                        69.1%; Score 1238.5; DB 10; Length 323; 69.3%; Pred. No. 8.9e-104; Live 31; Mismatches 51; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Van Damme B.J., Willems P., Peumans W.;
Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M94105; AAA32641.1;
HSSP; P23951; 2BAA.
                                                                                                                                                                                                                             ENDOCHITINASE,
1C85B6227A33EB06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 RYCDIFGIGYGNNLDCYNQLSFN 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 RYCDMLGVSYGANLDCYNQRPFN 322
                                                                                                                                                                                                                                      33764 MW;
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                             323
                                                                                                                                                                                                                                     323 AA;
                                                                                                                                                                                                                                                                                 Similarity
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Best Local Simi
Matches 224;
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SEQUENCE
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GGG------GVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 PSCHDVIIGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDI 299
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                    12 VLAVVLAAAAVTPATABQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGFRCQSQCTGCGG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 PSCHAVATGQWQPSAADQAAGRVPGFGVITNIINGGVECGHGSDTHVADRIGYYKRYCDL 301
                                                                                                                                                                                                                                                                                                                                                                                          120 TTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allium sativum (Garlic).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
                                                                                                                                                                                                                                                                                                                                               Indels 12;
                                                                                                                                                                                                                                                                                                                 Length 318;
                                                                                                                                                                                                                      POTENTIAL.
CHITINASE.
; 097C3DBD772468D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Damme E.V., Willems P., Peumans W.;
Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
EMBL, M94106, AAA32640.1;
EMBL, M94106, AAA32640.1;
EMBL, P23951, 2BAA.
Mendel; 704; Allsa;Chial;704.
Mendel; 704; PR001002; Chitin_bind.
InterPro; IPR001705; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19;
Pfam; PR00182; CHITINBINDNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   038776;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                       67.7%; Score 1213; DB 10;
66.9%; Pred. No. 1.7e-101;
tive 39; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 AA
InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19.
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
Chitin_binding; Signal.
NON_TER
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                                                                                                                                                                                                                                      18 318 C
318 AA; 33175 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 FGIGYGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 LQVGYGDNLDCGNQAHF 318
                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE PRECURSOR (EC 3.2.1.14) (CHITIODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 VASIVSRDLFERFILHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 GQISHETIGGWPIAPDGPPSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTH 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTAR 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSAAGRVPGYGVIINVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLS 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                            16 VLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGGGGGG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VLIFFALFINSYAQQCGSQGSGALCSNGLCCSQYGYCGNGGPYCGTGCQSQCGGPGGGSSG
                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                        Length 302;
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                     D0687D330BFFD75F CRC64;
                                                                                                                                                                                                                                                                      67.2%; Score 1204; DB 10;
69.4%; Pred. No. 1.1e-100;
iive 33; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 AA.
ProDom; PD000574; Glyco_hydro_19; 1.
SMART: SM00270; ChtBD1; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
PROSITE; PS00726; CHITIN_BINDING; 1.
Chitin-binding; Signal.
NON TER 1 17 POTENTIAL.
                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                       31728 MW;
                                                                                                                                                                                                                                                                      Query Match 67.2%, Best Local Similarity 69.4%, Matches 209; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 ------GCGGGGGGVASIVSRDLFERFILHRNDAACLARGFYTYDAFLAAAGAFPAF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 QLRRRRPDRPSGGGGSGVASIVSRSLFPDQMLLHRNDAACPAKNIYTYDAFVAAANAFPTF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTIGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ----GSPPSYCDQS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQSNKPSCHDVITGLWIPIARDSAAGRVPGYGVIINVINGGIECGMGQNDKVADRIGFYK 294
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                   9 ATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCT- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT
                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                Length 322;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                           SEQUENCE 322 AA; 34505 MW; AD56FE9CF7D99B09 CRC64;
                                                                                                                                                                                                                                                           Query Match 66.5%; Score 1192; DB 10; Best Local Similarity 67.2%; Pred. No. 1.4e-99; Matches 217; Conservative 30; Mismatches 56;
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom: PD000609; Chitin_bind; 1.
PROSITE; SM00270; Chtbbl; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
Chitin-binding; Glycosidase; Hydrolase; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002, 18:47:01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RYCDIFGIGYGNNLDCYNQLSFN 317
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Job time: 885 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein 3, 2002, 18:30:30 ; Search time 117.39 Seconds (without alignments) 201.290 Million cell updates/sec May Run on:

US-09-534-229C-3 Title:

1765 1 MRGVVVVAMLAAAFAVSÄHA......DLLGVSYGDNLDCXNQRPFA 319 Perfect score: Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 Total number of hits satisfying chosen parameters:

522463 seqs, 74073290 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

| SIDS2/gcgdata/geneseqp/AA1980.DAT:*
| SIDS2/gcgdata/geneseqp/AA1981.DAT:*
| SIDS2/gcgdata/geneseqp/AA1982.DAT:*
| SIDS2/gcgdata/geneseqp/AA1983.DAT:*
| SIDS2/gcgdata/geneseqp/AA1983.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Wheat chitinase pr	Rye chitinase-like	Rye chitinase-like	RCH10 chitinase pr	Rice chitinase. 0	Wheat chitinase pr	Amino acid sequenc	Basic chitinase 48	Chitinase encoded	Tobacco intracellu	Nicotlana sp. intr
SUMMARIES	AAB11489	AAW98079	AAW98080	AAR29019	AAR67969	AAB11488	AAB67444	AAR15841	AAR11305	AAR13275	AAW31297
DB	22	20	20	13	16	22	22	12	12	12	18
& Query Match Length DB 1	319	318	298	336	336	323	336	329	331	324	324
% Query Match	100.0	95.7	90.5	73.7	73.7	73.3	73.2	72.0	71.2	70.9	70.9
Score	1765	1688.5	1597.5	1301.5	1301.5	1294.5	1291.5	1270.5	1256.5	1252	1252
Result No.		7	m	4	Ŋ	9	7	80	σ	10	11

12	,	70.9	324	21	AAB07513	Amino acid sequenc
7 .	7 1	1.00	070	0 I	AAR20622	seduence or engocii
14	П	68.1	329	12	AAR56860	rnas
17	_	9.79	317	17	AAW00186	American elm chiti
16		65.5	292	18	AAW24554	Chitinase. Cucurb
17		64.2	303	13	AAR20820	Sequence of a 302
18		63.7	266	15	AAR52577	Chitinase G. Hord
19	1066	60.4	328	1.9	AAW64776	Floral organ-speci
20		56.8	2466	20	AAY05844	Banana ripening fr
21		52.5	243	20	AAW90169	C. ensiformis chit
22		45.6	254	12	AAR13274	Petunia extracellu
23		45.6	254	18	AAW31296	Petunia hybrida ex
24		45.6	254	21	AAB07512	Amino acid sequenc
25		45.6	284	21	AAB18905	A maize chitinase
26		45.0	439	3	AAR28150	Sugar beet chitina
27		44.6	272	21	AAG28415	Arabidopsis thalia
28		44.6	280	2.1	AAG28414	Arabidopsis thalia
29		44.1	253	16	AAR76714	Tobacco endochitin
30		4.	259	21	AAB18902	A maize chitinase
31		43.6	252	21	AAB18903	A maize chitinase
32		42.9	252	30	AAW98081	Rye chitinase-like
33			230	30	AAW98082	Rye chitinase-like
34			256	22	AAB11487	Wheat chitinase pr
35			372	22	AAB28788	Protein encoded by
36			250	16	AAR76713	Wild tomato endoch
37		o.	253	16	AAR76712	Wild tomato endoch
B		Š.	281	21	AAB18894	A maize chitinase
ω φ,		4	155	21	AAB18906	Amino acid sequenc
40		4	271	21	AAB18904	A maize chitinase
41		4	271	27	AAB18936	
7		ω,	268	13	AAR28147	Sugar beet chitina
43		ä	264	E 7	AAR28145	Sugar beet chitina
44		29.2	261	21	AAB18896	A maize chitinase
45		ω.	813	21	AAG53657	Arabidopsis thalia

ALIGNMENTS

RESULT

Wheat, chitinase, low temperature expression; hardened; plant, snow mould resistance; psychophilic plant pathogen; spring wheat. Wheat chitinase protein homologous to spring wheat chitinase. AAB11489 standard; protein; 319 AA. (first entry) Triticum aestivum. JP2000270866-A. 03-OCT-2000. 02-MAR-2001 AAB11489; AAB11489

99JP-0081694. 25-MAR-1999; (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.

99JP-0081694.

25-MAR-1999;

WPI; 2001-027417/04.

New low temperature expression chitinase gene for producing a plant grade highly resistant to psychophilic plant pathogenic microbes

Claim 7; Fig 3; 11pp; Japanese.

This invention describes novel wheat chitinase genes. The invention also describes a method for the isolation of a low temperature expression

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AAW98080;
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                                                                                                                                                                                                              181
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ID AAW9
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  0;
chitinase gene in which the mRNA is extracted from a fully hardened autumn wheat P1173438 (of high snow mould resistance). The genes are useful for creating a plant grade, highly resistant to psychophilic plant pathogenic microbes.
                                                                                                                                                                                                             ATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTFSSQWP 180
                                                                                                                                                                             241 KPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGDGRVADRIGFYKRYCD 300
                                                                                                                                  GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGF 120
                                                                                                             Gaps
                                                                                                  1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
                                                                                                                                                                                                                                                                                                                                                                                             CHT9; chitinase-like protein; antifreeze protein; AFP;
winter rye; antifungal; fungicide; cold tolerance; frost tolerance:
transgenic plant; preservation; cryopreservation; tumour; therapy.
                                                                                                                                                                                                    CAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..20
/note= "signal peptide"
21..318
/note= "mature protein, also claimed in Claim 10"
                                                                                  .,
                                                                 Length 319;
                                                                                  Indels
                                                                 Score 1765; DB 22;
Pred. No. 1.1e-137;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                             Rye chitinase-like protein CHT9 preprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xiong F;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moffatt B,
                                                                                                                                                                                                                                                                                                                            AAW98079 standard; Protein; 318
                                                                                  6
                                                                  100.0%;
ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                    301 LLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                             97US-0903B72.
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ICEB-) ICE BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hew C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-153795/13.
N-PSDB; AAX24889.
                                                                  Query Match
Best Local Similarity
Matches 319; Conserv
                                          319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               Secale cereale.
                                                                                                                                                                                                                                                                                                                                                            21-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09906565-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Griffith M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-FEB-1999
                                                                                                                                                                                                                                                                                                                                             AAW98079;
                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                   61
                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                    AAW98079
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The present sequence is winter rye (Secale cereal L. cv. Muskateer)
CHT9 preprotein. The mature protein, which is also claimed, is a
Chitianse-like protein that has chitimes (antifungal) and
antifreeze activities. CHT9 cDNA (see AAXA889) was obtained by
isolating mRNA from rye plants grown at low temperatures in the
abstract of pathogens of other stresses, i.e. under conditions when
only chitimases with antifreeze activity would be expressed. CHT9
and CHT46 (see AAW880B1-82) have been cloned and expressed in
Datterial and yeart (Pichia) systems and in Arabidopsis thaliana.
The chitimase-like antifreeze proteins can be used: to increase
freezing tolerance of plants and microorganisms to increase field
survival of plants, animals and microorganisms exposed to sub-zero
temperatures; to inhibit ice recrystallisation in biological
materials or foods; for cryopreservation and Mypotherature
of cells, embryos, tissues etc. (particularly human platelets); and
to kill tumour cells. They are also used to inhibit initiation and
properserved biological material. The signal peptide can be used
to to direct protein secretion in transgenic organisms or expression
everages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 KPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
New nucleic acid encoding antifreeze polypeptides from plants -
particularly with chitinase activity, used to impart frost, and
pathogen, resistant to plants, for preservation of foods, cells etc.
and for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALMFWMIPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1688.5; DB 20
Pred. No. 2.1e-131;
9; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW98080 standard; Protein; 298 AA.
                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rye chitinase-like protein CHT9.
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                        Claim 10; Fig 21a; 118pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 304;
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Tue May

240 agrvpgygvitniingglecgrggdarvadrigfykrycdllgvsygdnldcyngrpfa 298

AAR29019

qq

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cobtained by isolating mRRA from tree plants grown at low temperatures ochtained by isolating mRRA from rep plants grown at low temperatures in the absence of pathogens or other stresses, i.e. under conditions in the absence of pathogens or other stresses, i.e. under conditions of the childrases with antifreeze activity would be expressed. CHT9 and CHT46 (see AAN9908182) have been cloned and expressed in bacterial and yeast (Pichia) systems and in Arabidopsis thaliana. The childrase-like antifreeze proteins can be used; to increase field survival of plants, animals and microorganisms; to increase field survival of plants, animals and microorganisms exposed to sub-zero temperatures; to inhibit ice recrystallisation in biological materials or foods; for cryopreservation and hypothermic protection of cells, embryos, tissues etc. (particularly human platelets); and progression of diseases or spoilage caused by low temperature pathogens (particularly fungi) in plants, frozen foods and any cryopreserved biological material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding antifreeze polypeptides from plants - particularly with chitinase activity, used to impart frost, and pathogen, resistant to plants, for preservation of foods, cells etc. and for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is winter rye (Secale cereal L. cv. Muskateer) CHT9 mature protein. It lacks the 20-amino acid signal peptide of the preprotein (see AAW98079), which is also claimed. Mature CHT is a chitinase-like protein that has chitinase (antifugal) and antifreeze activities. CHT9 preprotein cDNA (see AAX24889) was
winter rye, antifungal; fungicide; cold tolerance; frost tolerance; transgenic plant; preservation; cryopreservation; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Fig 21d; 118pp; English.
                                                                                                                                                                                                                                                                                                   (ICEB-) ICE BIOTECH INC
                                                                                                                                                                                                                                                                                                                                           Griffith M, Hew C,
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-153795/13
                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAX24889.
                                                                           Secale cereale.
                                                                                                                     WO9906565-A2
                                                                                                                                                                                                                                                      31-JUL-1997;
                                                                                                                                                                                                          31-JUL-1998;
                                                                                                                                                               11-FEB-1999
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Xlong F;

Moffatt B,

98WO-CA00745. 97US-0903872. Mature CHT9

;; 141 SHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKKYFGRGPIQISHNYN 200 201 YGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHDVITGRWSPSGADQA 260 81 IISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGSTDVKKREVAAFLAQT 140 AGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSYGDNLDCYNQRPFA 319 Gaps 1 eqcgsqaggatcpnclccskfgfcgstseycgdgcqsqcnrc-ggtpvpvptptgggvss 59 EQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGCSGGTPVPVPTPSGGGVSS 1; DB 20; Length 298; 5; Indels 90.5%; Score 1597.5; DB 20 95.0%; Pred. No. 6.3e-124; live 9; Mismatches 5; Ouery Match Best Local Similarity 95.0° Matches 284; Conservative 180 21 9 120 261 ΩŽ qq Ω ŏ qq δà Q

Seguence

4;

The sequence given is encoded by the rice chitinase gene. The promoter region of this gene (see AAQ31407) is responsive to physical and/or biological stress. The pattern of expression of this protein in mature plants is characteristic. There is a low level of expression in mature leaves, a moderate level in plant stems and the highest level in roots and the male and female parts of the plant. The chitinase promoter sequence may be linked to a reporter gene for expression in mono- or dicotyledon plants. Expression of this reporter gene may be used to study patterns of development and controlled expression of plant defence genes and selectable genes. 60 N-----GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVA 112 61 srlrrrrpdasgg-----ggsgyasivsrslfdlmllhrndaacpasnfytydafva 112 113 AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD 171 17; Gaps 1 MRGVVVVVAMLAAAF-AVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC 59 /note= "Region conserved between class I and class II chitinases" i. Promoter; region; rice; chitinase; physical; biological; stress; Length 336; DNA fragment contg. chitinase gene and its regulatory region responsive to mature plant stress and has low level expression leaves, moderate level expression in stem and high level expression in roots leaves; stems; roots; male; female; reporter; monocotyledon; dicotyledon; development; plant; defence; selectable; genes. 47; Indels Score 1301.5; DB 13; Pred. No. 1.8e-99; 27; Mismatches Disclosure; Page 33-34; 45pp; English. (SALK) SALK INST BIOLOGICAL STUDIES Location/Qualifiers Ā AAR29019 standard; Protein; 336 73.78; 91US-0704288 Conservative RCH10 chitinase protein WPI; 1992-415785/50. Similarity 336 AA; N-PSDB; AAQ31407 Zhu Q; Oryza sativa. Query Match Best Local Simi Matches 237; 22-MAY-1991; WO9220807-A 20-APR-1993 26-NOV-1992 Sequence Lamb CJ, AAR29019; Region g δλ g ŏ

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--ggsgvasivsrslfdlmllhrndaacpasnfytydafva 112
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                                                                                                                                                                                                                                                                                                                                                   99JP-0081694
                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                            snow mould resistance;
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-027417/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogenic microbes
 srlrrrrpdasgg-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 AA;
                                                                                                                                                                                                                                                                    Wheat; chitinase;
                                                                                                                                                                                                                                                                                               Triticum aestivum.
                                                                                                                                                                                                                                                                                                               JP2000270866-A.
                                                                                                                                                                                                                                                                                                                                                    25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                       25-MAR-1999;
                                                                                                                                                                                                                               02-MAR-2001
                                                                                                                                                                                                                                                                                                                                 03-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                              AAB11488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local
Matches 22
                                                                                                                                                                          9
                                                                                                                                               293
                   113
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61
                                                                                                                             292
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                                                                                                                                                                         RESULT
AAB11488
                                                                                                                                                                                                               QC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 N-----GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVA 112
                                       291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRGVVVVAMLAAAF-AVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The SphI fragment of rice chitinase RCH10 gene (given in AAQ81346) an alfalfa beta-1.3-glucanase coding sequence (AAQ81347) were incorporated into vectors for co-expression in transgenic tobacco, resulting in improved resistance to Cercospora nicotinae and Thanatephorus cucumeris fungal infection.
WFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADR
                            YCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic plants contg. several plant defence associated proteins - have increased resistance to plant pathogens when
                                                                                                                                                                                                                                       Chitinase; transgenic plant; disease resistance;
crop improvement; tobacco; Nicotiana tabacum; plant defense;
fungus pathogen; Cercospora nicotinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1301.5; DB lb;
Pred. No. 1.8e-99;
---rhes 47;
                                                                                                                                                                                                                                                                                                                                                                                                 Zhu Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 31-32; 45pp; English.
                                                                                                             IGFYRRYCDLLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                                                                                                              (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                   Ä.
                                                                                                                                                                AAR67969 standard; Protein; 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                             grown in crops as a food source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                 EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.7%;
72.3%;
                                                                                                                                                                                                                                                                                                                                                            93US-0093372.
                                                                                                                                                                                                                                                                                                                                                                                                 Maher
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                     Thanatephorus cucumeris
                                                                                                                                                                                                                                                                                                                                                                                                Lamb CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-067090/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ81346.
                                                                                                                                                                                                                       Rice chitinase.
                                                                                                                                                                                                                                                                                     Oryza sativa
                                                                                                                                                                                                                                                                                                                                           15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                            16-JUL-1993;
                                                                                                                                                                                                     13-AUG-1995
                                                                                                                                                                                                                                                                                                     WO9502319-A.
                                                                                                                                                                                                                                                                                                                         26-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237;
                                                                                                                                                                                                                                                                                                                                                                                                 Dixon RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                   AAR67969:
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Matches
                                                                                                   292
          113
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This invention describes novel wheat chitinase genes. The invention also describes a method for the isolation of a low temperature expression chitinase gene in which the mRNA is extracted from a fully hardened autumn wheat P1173438 (of high snow mould resistance). The genes are useful for creating a plant grade, highly resistant to psychophilic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New low temperature expression chitinase gene for producing a plant grade highly resistant to psychophilic plant pathogenic microbes
                                                                                                                            YCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTAL
                                                                                                                                                                                                232 WFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 VVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGCSG
AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  low temperature expression; hardened; nnce; psychophilic plant pathogen; rye.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dred. No. 6.6e-99; i Mismatches 48: Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wheat chitinase protein homologous to rye chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.3%; Score 1294.5; 71.0%; Pred. No. 6.6e
                                                                                                                                                                                                                                                                                                                               IGFYKRYCDLLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB11488 standard; protein; 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a chitinase designated RCHIO. The specification describes chimeric receptors which are used for modulating plant responses to pathogens. The receptors comprise a heterologous extracellular domain (e.g. from a Bril protein or RCHIO protein) and a kinase domain (e.g. from disease resistance protein Xa21). The Xa21 gene is a member of disease resistance protein Xa21). The Xa21 when Xa21 is present in a transgenic plant, it confers resistance to Xanthomonas spp.. The plant receptors containing heterologous domains are useful for modulating plant responses to pathogens including viruses, bacteria, nematodes, fungi or insects. The nucleic acids can be used to
                                                                                                                                                                                                                                                                                                                                                                        Disease resistance protein; Xa21; RKK gene; transgenic plant, chitinase; Xanthomonas; plant pathogen; Bril protein; RCH10 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric plant receptors comprising a polynucleotide encoding a RRK receptor containing a heterologous extracellular domain and a kinase domain from a Xa21 polypeptide, useful for modulating plant responses
                                                                 STDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPG 184
              KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS
                                                                                                           HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV
                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a rice chitinase designated RCH10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 confer desired traits on essentially any plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 45-46; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SALK INST BIOLOGICAL STUDIES
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                                                                                                                                                                                                                                                               AAB67444 standard; Protein; 336 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000; 2000WO-US20714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0363313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chory J,
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                           303 gygnnidcynglsf 316
                                                                                                                                                                 SYGDNLDCYNORPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-159858/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    He 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathogens
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                                                                                                                                                                                                                                                                                                                     15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ronald P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sp.
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                                                      185
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                                                                                                                                                                                                        N-----GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVA 112
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                      9
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srlrrrpdasgg-----ggsgvasivsrslfdlmllhrndaacpasnfytydafva
MRGVVVVVAMLAAAF-AVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC
                        1 mralavvamvarpflaaavhaeqcgsqaggavcpnclccsqfgwcgstsdycgagcgsqc
                                                                                               113 AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD
                                                                                                                                             YCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTAL
                                                                                                                                                                                          WFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence encoding vacuole targetting peptide - esp. signal region of tobacco chitinase or glucanase gene, and derived recombinant DNA, vectors, etc. functional in plants
                                                                                                                                                                                                                                                                                                                                                                                                                          Vacuole; targetting; chitinase; glucanase; signal; resistance; pharmaceutical; hormones; expression; secretion; extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= sig_peptide
/note= "used as vacuole targetting peptide"
                                                                                                                                                                                                                                                                                                                                                                                                  Basic chitinase 48 from clone lambdaCHN17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 64-68; 81pp; English
                                                                                                                                                                                                                                                           293 igfykrycdifgvsyganldcysgrpsa 320
                                                                                                                                                                                                                                           IGFYKRYCDLLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicotiana tabacum L. c.v. Havana 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= exonl_prod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= exon2-prod.
200..329
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318..329
                                                                                                                                                                                                                                                                                                                             AA
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                                                                                                                                                                                                                                                                                                                             AAR15841 standard; Protein; 329
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1991-371028/51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1991;
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Region
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Gaps

17;

Indels

73.2%; Score 1291.5; DB 22; 71.6%; Pred. No. 1.2e-98; Live 27; Mismatches 49; D

Conservative

Query Match Best Local Similarity Matches 235; Conserv

Length 336;

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EP440304-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR13275;
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                       126
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                                                                                                                                                                                                                                                                                                                                                                           DVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVS 305
                                                                                                                                                                                                                                                                  Ptp-ptppgggdlgsiisssmfdgmlkhrndnacqgkgfysynafinaarsfpgfgtsgd 127
Attachment of the signal peptide ensures occlusion of expressed prod. in the vacuole while elimination of the signal peptide from a sequence normally conty, it ensures that the expressed product is secreted into the extracellular space, rather than retained in the vacuole. Recombinant DNA may contain a structural gene which protects the plant, e.g. resistance to pathogens, herbicides, insecticides, biocides, environmental stress, etc.; leads to pharmaceuticals such as hormones or immunommodulators. See also ARQ15146-50 and ARQ15330-35.
                                                                                                                                                                                                  8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG -CQSQCNGCSGGT
                                                                                                                                                                                                             TDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNOERGATSDYCTPSSOWPCAPGK
                                                                                                                                                                                                                                                                                                                                 KYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSH
                                                                                                                                                                             5.
                                                                                                                                                       Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA regulatory sequence from new tobacco chitinase gene
                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant chitinase; transgenic plants; pathogen resistance
                                                                                                                                                       DB 12;
                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chitinase encoded by genomic clone lambda CHN17
                                                                                                                                                                    Pred. No. 6.4e-97
                                                                                                                                                       72.0%; Score 1270.5; 72.8%; Pred. No. 6.4e
                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                       306 YGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                          pgdnldcgngrsf 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meins F, Shinshi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-088356/13.
N-PSDB; AAQ11093.
                                                                                                                                                                 Similarity
                                                                                                                        329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 - MAR - 1991
                                                                                                                                                             Best Local Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP418695-A.
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR11305
                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            308
                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                     126
                                                                                                                                                                                                                                                                                                           128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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67 PVPVPTPSGGG-VSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 sllfsllllsasaeqcgsqaggarcpsglccskfgwcgntndycgpgncqsq---cpggp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 SHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSS-QWPCAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPS
                                                                                                                                This recombinant tobacco chitinase gene prod. is encoded by a genomic close, lambda CHNI7 which comprises 3 exons and has 5' - and 3' - untranslated regions. A fragment (claimed) from the 5'-untranslated region can be used to increase the ex-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 331;
                                                                                                                                                                                                                   pression of foreign genes in transgenic plants. The fragment is linked to a foreign gene, eg chithnase or glucanase gene via a spacer and is also linked to regulatory sequences. The resultant DNA construct is used to transform plant cells, eg tomato or tobacco, which subsequently produce the gene product at high level.
used to increase expression of foreign genes in transgeni
plants, partic for improving resistance to pathogens etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24..324
/label= intracellular chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 9.2e-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.2%; Score 1256.5; 72.1%; Pred. No. 9.2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR13275 standard; Protein; 324 AA
                                                                              65pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fungal resistance; phytopathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tobacco intracellular chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana tabacum Samsun NN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 227; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 VSYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || ||||||| ||| || || vspgdnldcgnqrsf 322
                                                                                Disclosure; page 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   See also AAQ11094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-OCT-1991
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Meulenhoff EJS,
  Nicotiana sp.
                                                                                                                                                                                              Vloemans AA,
                                                                                                              19-APR-1993;
                                                                                                                              29-JAN-1991;
                                                                          US5670706-A.
                                                                                            23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                             Peptide
                                                Protein
                                                                                                                                                                           Bol JF,
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
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                                                                                                                                                                                                                                                                                                        3,
                                                                                                                                                                                                                                                                                                                                                           PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                          99
                                                                                                                                                                      The sequence from which this amino acid was deduced was isolated from a N.tabacum Chalbrary following screening with a partial tobacco intracellular chitinase clone. The protein sequence appears twice in the specification but in one (not the one given in this file), the Leu codons at positions -23, -21, -15, -12, -11, -8, -7, -6, -5 and plus 16, 52, 65, 137, 176, 177, 182, 195, 228, 242, 266, 274, 286 are translated as Ile.
                                                                                                                                                                                                                                                                                                                     8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
                                                                                                                                                                                                                                                                                                                                 247 VIIGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY
                                                                                                                                                                                                                                                                                                                                                                                             127 DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK
                                                                                                                                                                                                                                                                                                                                                                                                        187 YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSFKPSSHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Intracellular chitinase; antifungal; transgenic plant; synergism; beta-1,3-glucanase gene; tobacco.
                                                                                                                                                                                                                                                                                                      8
                                                                                                                  Plants with improved resistance to pathogenic fungi - contains chitinase and/or beta-1,3-glucanase genes modified for over-expression targetted to apoplasts
                                                              Roekel JS;
JF;
                                                                                                                                                                                                                                                                                    Length 324;
                                                                                                                                                                                                                                                                                                      Indels
                                                                Van
Bol
                                                                                                                                                                                                                                                                                  70.9%; Score 1252; DB 12; 71.8%; Pred. No. 2.1e-95;
                                                                                                                                                                                                                                                                                           2.1e-95;
ches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intracellular chitinase protein.
                                                               Meulenhoff EJ,
Woloshuk CP,
                                                                                                                                                                                                                                                                                                    29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW31297 standard; Protein; 324 AA
                                                               Melchers LS, N
, Vloemans AA,
                                                                                                                                                     Example 4; Fig 2; 55pp; English.
                                   (MOGE-) MOGEN INT NV.
(UYLE-) RIJKSUNIV TE LEIDEN.
91EP-0200191
                   90NL-0000222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gdnldcgngrsf 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDNLDCYNQRPF 318
                                                                                        WPI; 1991-232019/32.
N-PSDB; AAQ12898.
                                                                                                                                                                                                                                      See AAQ12897-Q12900
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                        324 AA;
                                                                        Sela-Buurlage MB,
                                                               Cornelissen BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana sp.
30-JAN-1991;
                  30-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-1998
                                                                                                                                                                                                                                                                                                     Matches 224;
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW31297
                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                            69
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92
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to construct a transgenic plant in a novel method to produce plants resistant to fungal attack. Such transgenic plants expressing an intracellular plant chitinase gene and a plant beta-1,3-quucanase gene within its tissues are predicted to exhibit improved resistance to pathogenic fungi. Such genes should be operably linked to promoters and terminators and optionally a gene encoding a selectable or screenable trait. Plants that overexpress the chitinase and glucanase genes exhibit a synergistic antifungal effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents an intracellular chitinase which is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fungus-resistant transgenic plants - containing genes encoding intracellular chitinase and beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Melchers LS;
                                                                                                                                                                                                                                                                                                                                                                                                         Cornelissen BJC, Linthorst HJM, Melche: ff EJS, Sela-buurlage MB, Van ROEKEL JSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.9%; Score 1252; DB 18; 71.8%; Pred. No. 2.1e-95; ive 29; Mismatches 51;
                                                                                        "intracellular protein"
                      1..23
/label= signal_peptide
24..324
/note= "intracellular g
Location/Qualifiers
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                                                                                                                                                                                                                                         93US-0047413
                                                                                                                                                                                                                                                                                    91US-0647831
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Woloshuk CP;
                                                                                                                                                                                                                                                                                                                                  (MOGE-) MOGEN INT NV.
(UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 71.8
nes 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||||| ||| || || || gdn||dcgnqrsf 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDNLDCYNQRPF 318
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N-PSDB; AAT89952.
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247 VITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                      AAR20822 standard; Protein; 328 AA.
                                                                                                                                                                                                                                                                                                                                                                               25..69
/label= cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leguay JJ,
                                                                                                                                                                                                                                                                                                                                                       1..24
/label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SNFI ) SANOFI SA.
(ERAP ) SOC NAT ELF AQUITAINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 4; 82pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91WO-FR00607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90FR-0009460.
                                                                                                                                                                                                             (first entry)
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                                                      307 GDNLDCYNQRPF 318
                                                                              304 gdnldcgngrsf 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grison R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-064950/08.
N-PSDB; AAQ21193.
                                                                                                                                                                                                                                                                                                             Tomato and tobacco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 213; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 - JUL-1990;
                                                                                                                                                                                                             16-MAY-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dubois M,
                                                                                                                                                                                   AAR20822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                   nematode
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                                                                                                                                           AAR20822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents an extracellular chitinase. The specification describes transgenic plants which express a chitinase gene and a glucanase gene. The expression of the chitinase and beta-1,3-glucanase genes produces an antifungal effect. The transgenic plants are useful for improving plant resistance to pathogenic fungithe recombinant polynuclectides and the process are useful for producing fungal resistant plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transgenic plants expressing chitinase and glucanase have improved resistance against pathogenic fungi, particularly against Alternaria alternata or Fusarium oxysporum f. sp. lycopersici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 DVKKREVAAFLAQISHETIGGWPTAPDGPYSWGYCFNQERGAISDYCIPSSQWPCAPGKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD 246
                                                                                                                                                                                                                                                                                                                                                                                                                  Meulenhoff EJS, Sela-buurlage MB;
JF, Linthorst HJM, Van Roekel JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 324;
                                                                                                                    Chitinase; transgenic plant; beta-1,3-glucanase; antifungal; plant resistance; pathogenic fungi; fungal resistant plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                           Amino acid sequence of an extracellular chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1252; DB 21
Pred. No. 2.1e-95;
9; Mismatches 51
                                                                                                                                                                                                                      /note= "signal peptide"
                                                                                                                                                                                           Location/Qualifiers
          AAB07513 standard; Protein; 324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Fig 2A-B; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.9%; Scor
71.8%; Preditive 29;
                                                                                                                                                                                                                                                                                                                                                                                                                    Melchers LS,
oshuk CP, Bol
                                                                                                                                                                                                                                                                                                                                               91US-0647831,
                                                                                                                                                                                                                                                                                                        97US-0801563
                                                                                                                                                                                                                                                                                                                                  93US-0047413
                                                                                                                                                                                                                                                                                                                                                                                                                                  Woloshuk CP,
                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                       (UYLE-) RIJKSUNIV LEIDEN. (MOGE-) MOGEN INT NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-498214/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 224; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAA58910
                                                                                                                                                                                                                                                                                                                                                                                                                    Cornelissen BJC,
                                                                                                                                                               Nicotiana sp
                                                                                                                                                                                                                                                                                                                                                                                                                                  Vloemans AA,
                                                               20-0CT-2000
                                                                                                                                                                                                                                                                                                        18-FEB-1997;
                                                                                                                                                                                                                                                                                                                                  19-APR-1993;
                                                                                                                                                                                                                                                                                                                                                 29-JAN-1991;
                                                                                                                                                                                                                                                 US6087560-A.
                                                                                                                                                                                                                                                                           11-JUL-2000,
                                      AAB07513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
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The inventors claim a new recombinant gene which codes for a protein with encochitinase activity, or its precursor (see AAQ21007). The coding part of the gene contains at least the 5' part of DNA for tomato endochitinase and at least the 3' part of DNA for the tobacco enzyme (DNA can be genomic or CDNA, but at least one intron is prefigerable. The recombinant gene includes the 35s promoter of cauliflower mosaic virus plus the terminator from the nopaline synthase gene of Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 VAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pest-resistant plant; transformed plant; fungi; insect; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to fungi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant protein with endo chitinase activity -
encoding it and plants which express it, resistant to f
insects, bacteria and nematodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toppan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pignard A,
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317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0286020
                                                                                                          Query Match 68.1
Best Local Similarity 67.8
Matches 213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sticklen MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 spgdnldcgnqrsf 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fungal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT33325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        American elm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW00186;
                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                            127
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                                                                   244
                                                                                                                                       186 rkyfgrgpigishnynygpcgraigvdllnnpdlvatdpvisfktaiwfwmtpgspkpsc 245
                                                                                                                                                                                  66 TPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAK-GFYNYGAFVAAANSFSGFATTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence coding for wheat germin, a protein induced during germination of wheat, is a preferred example of DNA coding for a protein able to degrade oxalic acid. Such DNA can be coupled to a sequence of interest, e.g. one coding for enzymes which confer resistance to pathogens (esp. endochitinases). Plant calli which
              125 STDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPG
                                                                                                            KKYFGRGPIQISHNYNYGPAGQAIGIDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS
                                                                                                                                                                   HDVITGRWSPSGADQAAGRVPGYGVITANINGGLECGRGQDGRVADRIGFYKRYCDLLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant
                                                                                                                                                                                                                                                                                                                                                                                                                                      oxalic acid degradation; oxalate oxidase; selection marker; tomato endochitinase; tobacco endochitinase; precursor; pathogen resistance; plant cell selection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of gene encoding oxalic acid degrading enzyme - for placell selection, esp. gene coupled to gene-encoding protein conferring pathogen resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schneider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grezes-Besset B, Grison R, Pignard A,
                                                                                                                                                                                                                                                                                                                                                                                                            Endochitinase precursor coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25..75
/label= pro-sequence
76..329
/label= endochitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 34-37; 64pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..24
/label= pre-sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        AAR56860 standard; Protein; 329 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SNFI ) ELF SANOFI.
(ERAP ) SOC NAT ELF AQUITAINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-FR01203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92FR-0014721
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lycopersicon esculentum
Nicotiana tabacum.
                                                                                                                                                                                                                         305 SYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                          WPI; 1994-217870/26.
N-PSDB; AAQ68352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                    AAR56860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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Region

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244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 TPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAK-GFYNYGAFVAAANSFSGFATTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                    184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV 304
                                                                                                                                                                                                                                          11; Gaps
                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                          67
have been successfully transformed by the sequences are selected by their ability to grow on oxalic acid-contg. medium. AAR56860 is a known sequence of a precursor of endochitinase; the sequence was previously disclosed in W09201192.
                                                                                                                                                                                                                                                                                                                      125 STDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPG
                                                                                                                                                                                                                                                                                            7 VAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS
                                                                                                                                                                                            DB 15; Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone pHS2; chitinase; american elm; fungus; Ophiostoma ulmi; dutch elm disease; E. coli; chitinase-like protein;
                                                                                                                                                                                            68.1%; Score 1202.5; DB 15; Lengt. 67.8%; Pred. No. 2.6e-91; ive 38; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Mature chitinase-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       American elm chitinase-like protein.
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This sequence is encoded by the cDNA clone pHS2, and represents a protein having chitinase-activity derived from american elm. This protein inhibits the fungus Ophiostoma ulmi, the causative agent of dutch elm disease. The clone pHS2 may be used to transform E. coli cells for the recombinant production of the chitinase-like protein. The protein may be used in a composition to inhibit fungal infection of elm trees.
                  Isolated chitinase gene derived from an American elm - used obtain prods. for inhibiting fungal infection of plants
                                                                                    Claim 1; Fig 1; 12pp; English.
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Sequence 317 AA;

., 140 TSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTFSSQWPCAPGKKYFGRGFIQISHNY 199 nygqcgraiganllonpdlvatdpvisfktalwfwmtpqspkpschdvitgrwspsgtdq 249 SIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGSTDVKKREVAAFLAQ 139 NYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHDVITGRWSPSGADQ 259 260 AAGRVPGYGVIINIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSYGDNLDCYNQRPF 318 11; Gaps 20 AEQCGSQAGGATCPNCLCCSKFGFCGTTSDXCGTGCQSQCNGCSGGTPVPVPTPSGGGVS 79 67.6%; Score 1192.5; DB 17; Length 317; 70.6%; Pred. No. 1.7e-90; Live 30; Mismatches 47; Indels 11; Query Match 67.6% Best Local Similarity 70.6% Matches 211; Conservative 130 80 200 190 250 q δŏ ð g qq δy QQ δÃ ŏ

3, 2002, 18:30:32 Search completed: May Job time: 7551 sec

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Sequence 2, Appli
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Sequence 11
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1 MRGVVVVAMLAAAFAVSAHA......DLLGVSYGDNLDCYNQRPFA
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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           Compugen Ltd
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US-08-448-398-3
GenCore version 4.5
Copyright (c) 1993 - 2000 Comy
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Sequence 4, Appli
Sequence 17, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ELEMENTS
TITLE OF INVENTION: ELEMENTS
TITLE OF INVENTION: ELEMENTS
TO SEQUENCES: 26
CORRESPONDENCE 126
CORRESPONDENCE ADDRESS:
ADDRESSE: PRETIY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 44 South Flower Street, Suite 2000
CITY: Los Angels
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRGVVVVVAMLAAAF-AVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPSRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/07/704,288C
FILING DATE: VAY-1991
CLASSIFICATION: 800
US-08-047-413-9
US-08-229-050-9
US-08-229-050-9
US-07-791-931-8
US-07-791-931-9
US-08-162-475A-5
US-08-162-475A-4
US-08-162-153-158-158-158-14
US-08-329-799-359-15
US-08-379-259-14
US-08-379-259-14
US-08-379-259-14
US-08-379-259-14
US-08-379-259-14
US-08-379-259-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/07704288C; Patent No. 5399680; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LAMB, CHRISTOPHER J. APPLICANT: ZHU, QUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3:
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amino acid
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Best Local Similarity 72.3
Matches 237; Conservative
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; MOLECULE TYPE: protein
US-07-704-288C-3
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     US-07-704-288C-3
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SRIRRRRPDASGG------GGSGVASIVSRSLFDLMLJHRNDAACPASNFYIYDAFVA 112
N-----GCSGGTPVPVPTFSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVA 112
                                                                                                                                                                                113 AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD
                                                                                                                                                               YCTPSSQWPCAPGKKYFGRGFIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
TITLE OF INVENTION: BLEENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.7%; Score 1301.5; DB 1
72.3%; Pred. No. 5.8e-111;
tive 27; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PROOR APPLICATION DATE:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
                                                                                                                                                                                                                                                                                                                                 292 IGFYKRYCDLLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                                                                                      293 IGFYKRYCDILGVSYGANLDCYSQRPSA 320
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REFERENCE/DOCKET NUMBER: P31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELERAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08379259 Patent No. 5695939
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CORRESPONDENCE ADDRESS
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CITY: Los Angeles
STATE: California
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Best Local Similarity
Matches 237; Conserv
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US-08-379-259-3
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US-08-379-259-3
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                                                                                                         YCQQSAQWPCAAGKKYYGRGPIQLSYNFNYGPAGQAIGADLLGDPDLVASDATVSFDTAF 232
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                            -----GGSGVASIVSRSLFDLMLLHRNDAACPASNFYTYDAFVA
                                                                               113 AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD
                                                                                                                                                               YCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lamb, Christopher J.
APPLICANT: Zhu, Qun
APPLICANT: Aber, Elleen A.
APPLICANT: Maher, Elleen A.
APPLICANT: Maher, Elleen A.
TITLE OF INVENTION: TRANSCENIC PLANTS CONTAINING MULTIPLE TITLE OF INVENTION: DISEASE RESISTANCE GENES
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,372
FILING DATE: 16-JUL-1993
CLASSIFICATION: 800
ATORNEY/AGENT INFORMATION:
NAME: Relier, Stephen E.
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: 31,192
REGISTRATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: Pretty, Schroeder, Brueggemann & Clark
1: 444 South Flower Street, Suite 2000
Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.7%; Score 1301.5; DB 1
72.3%; Pred. No. 5.8e-111;
tive 27; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                        293 IGFYKRYCDILGVSYGANLDCYSQRPSA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08093372
Patent No. 5530187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 72.35
Matches 237; Conservative
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; MOLECULE TYPE: protein
US-08-093-372-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COUNTRY: U.S.A.
ZIP: 90071-2921
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CITY: Lo
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US-08-093-372-2
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COMPUTER READMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,413
FILING DATE: 19-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.9%; Score 1252; DB 1;
71.8%; Pred. No. 1.8e-106;
Live 29; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24615-20022.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/647,831 FILING DATE: 29-JAN-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          E: Morrison & Foerster 755 Page Mill Road
                            Sequence 11, Application US/08047413
Patent No. 5670706
GENERAL INFORMATION:
APPLICANT: Cornelissen, Bernardu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATECHMENT MARSHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2461
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 324 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19 CLASSIFICATION:
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STREET: 75
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              US-08-047-413-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 AFLAQTSHETTGGWPTAPDGPYSWGYCENQERGATSDYCTPSSQWPCAPGKKYFGRGPIQ 194
                                                                                                                                                                        YCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTAL 231
                                                                                                                                                                                                                                                                                                    232 WFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADR 291
                                                                        N-----GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVA 112
                                                                                                                                                113 AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 VSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGTPVPVPTPS 74
                                  1 MRALAVVAMVARPFLAAAVHAEQCGSQAGGAVCPNCLCCSQFGWCGSTSDYCGAGCQSQC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 ISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHDVITGRWSP
1 MRGVVVVAMLAAAF-AVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Raikhel, Natasha V.
TITLE OF INVENTION: Nettle Lectin CDNA
FILE REFERENCE: MSU 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
SOFWBARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                  292 IGFYKRYCDLLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                                                                                                                                    293 IGFYKRYCDILGVSYGANLDCYSQRPSA 320
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; Sequence 6, Application US/07791931C
; Patent No. 6133507
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Nicotiana tabacum
US-07-791-931-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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APPLICANT: Cornelissen, Bernardus J.C.
APPLICANT: Meulenhoff, Elisabeth J.S.
APPLICANT: Meulenhoff, Elisabeth J.S.
APPLICANT: Van Roekel, Jercen S.C.
APPLICANT: Sela-Buurlage, Marianne B.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Bol, John F.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: PROCESS FOR
TITLE OF INVENTION: OBTAINING FONGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
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APPLICANT: Cornelissen, Bernardus J.C.
APPLICANT: Melchers, Leo S.
APPLICANT: Melchers, Leo S.
APPLICANT: Melchers, Leo S.
APPLICANT: Weulenhoff, Elsabeth J.S.
APPLICANT: van Roekel, Jeroen S.C.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Wloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: GUNGAL RESISTANT PLANTS, PROCESS FOR TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT TITLE OF INVENTION: POLYNCECTIDES FOR USE THEREIN
187 YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD 246
                                                                                                                                                                                                                                          247 VITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
                                                                                                                                                                                                                                                                 127 DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/801,563 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24615-20022.00
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19-APR-1993
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MITASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08801563 Patent No. 6087560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morrison & Foerster
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 324 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415-494-0792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                            304 GDNLDCGNQRSF 315
                                                                                                                                                                                                                                                                                                                               307 GDNLDCYNQRPF 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Cornel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 410 TELEFAX: 706141
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Patent No. 6066491

Setent No. 6066491

APLICANT: Cornelissen, Bernardus J.C.

APPLICANT: Melchers, Leo S.

APPLICANT: Melchers, Leo S.

APPLICANT: Welchers, Jeroen S.C.

APPLICANT: Vloemans, Alexandra A.

APPLICANT: Vloemans, Alexandra A.

APPLICANT: Woloshuk, Charles P.

APPLICANT: Woloshuk, Charles P.

APPLICANT: Linthorst, Hubertus J.M.

TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR

TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT

TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT

TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
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                           247 VITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
                                                    Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 1252; DB 3;
; Pred. No. 1.8e-106;
29; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24615-20022.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-7AN-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 71.8
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-229-050-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 755 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 800
                                                                                                                                        304 GDNLDCGNQRSF 315
                                                                                                               GDNLDCYNQRPF 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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                                                                                                                                                                                                                        RESULT 6
US-08-229-050-11
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75 GGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGSTDVKKREVA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                        255 SGADQAAGRVPCYGVIINIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSYGDNLDCYN 314
                                                                                                                                                                                                                                                                       AFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKKYFGRGPIQ 194
                                                                                                                       16 VSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGTPVPVPTPS 74
                                                                                                                                          70.6%; Score 1246.5; DB 1; Length 310; 73.7%; Pred. No. 5.4e-106; Live 26; Mismatches 45; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ZHU, QUN
TITLE OF INVENTION: DEFENSE GENES AND PLANT
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSES: PERTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5695939
GENERAL INFORMATION:
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TELEPHONE: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 444 South Flower
CITY: Los Angeles
STATE: California
COUNTRY: United States
ZIP: 90071-2921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619) 546-9392
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SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acid
                                                                    Best_Local Similarity 73.7:
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 ORPF 318
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US-07-704-288C-6
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US-08-379-259-6
                                                    Query Match
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                                                                                                                                                                                                                                                                                                   187 YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD 246
                                                                                                                                                                                                                                                                                                                                                                             247 VIIGRWSPSGADQAAGRVPGYGVIINIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY TITLE OF INVENTION: ELEMENTS NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       67 PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                      Gaps
                                                                                                                             8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT 66
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                                                      Length 324;
                                                                                           Indels
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et, Suite 2000
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
                                                      Score 1252; DB 3;
Pred. No. 1.8e-106;
                                                                                           29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
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TELEFAX: (619) 546-9392
                                                      70.9%;
71.8%;
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COUNTRY: United States
ZIP: 90071-2921
COMPUTER READABLE FORM:
                                                                                             Conservative
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MOLECULE TYPE: protein
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                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                           Matches 224;
     US-08-801-563-11
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Recombinant gene coding for a protein having endochitinase activity or for a precursor thereof. 15
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184 PGRKYFGRGPIQISHNYNYGPCGRAIGVDLLNNPDLVATDPVISFKTALWFWMTPQSPKP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGG
                                                       244 SCHDVIIGRWNPSSADRAANRLPGFGVITNIINGGLECGRGTDNRVQDRIGFYRRYCSIL
                                      SSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/842,165
FILING DATE: 01-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00607
FILING DATE: 21-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90 09460
FILING DATE: 24-JUL-1990
ATTOREX/ASPRT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16781/564/BEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: Foley & Lardner: 3000 K Street, N.W., Suite 500 Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                       APPLICANT: DUBOIS, Michel.
APPLICANT: GRISON, Rene
APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant 96
TITLE OF INVENTION: Alain
TITLE OF INVENTION: Alain
                                                                                                                                                                                                                                                            Sequence 13, Application US/08475427 Patent No. 5859340 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 67.8
Matches 213; Conservative
                                                                                                                       GVSYGDNLDCYNQRPF 318
                                                                                                                                                                304 GVTPGDNLDCVNQRWF 319
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US-08-475-427-13
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                                                                                                                                                                                                                                                                                                                                                                                                                 75 GGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGSTDVKKREVA 134
                                                                                                                                                                                                                                                                                                                                  135 AFLAQISHETIGGWPTAPDGPYSWGYCFNQERGAISDYCTPSSQWPCAPGKKYFGRGPIQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 ISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHDVITGRWSP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGADOAAGRVPGYGVITNIINGGLECGRGODGRVADRIGFYKRYCDLLGVSYGDNLDCYN 314
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                                                                                                                                                                                       Gaps
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                                                                                                                                               DB 1; Length 310;
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                                                                                                                                                                                       Indels
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; Pred. No. 1.9e-102;
31; Mismatches 57;
                                                                                                                                          ; Score 1246.5; DB 1;
; Pred. No. 5.4e-106;
26; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Raikhel, Natasha V.
TITLE OF INVENTION: Nettle Lectin CDNA
FILE REFERENCE: MSU 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/07791931C Patent No. 6133507 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 68.4%;
Best Local Similarity 69.0%;
Matches 218; Conservative 31
                                                                                                                                                 70.6%;
73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OMGANISM: Solanum tuberosum
US-07-791-931-5
                                                                                                                                               Query Match
Best Local Similarity 73.73
Matches 224; Conservative
        TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                              TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-379-259-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 QRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 QRSF 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-791-931-5
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APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS 244
                                        66 TPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAK-GFYNYGAFVAAANSFSGFAITG 124
                                                                                                                      SIDVKKREVAAFLAQISHETIGGWPIAPDGPYSWGYCFNQERGAISDYCTPSSQWPCAPG 184
                                                                                                                                                                                                                                                                                    245 HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV 304
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16 LVLLSAAL----AQNCGSQGGGKVCASGQCCSKFGWCGNTNDHCGSGNCQSQ---CPGG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: PRETIY, SCHROEDER, BRUEGGEMANN & CLARK 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/07/704.986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 68.1%; Score 1202; DB 1; Best Local Similarity 68.7%; Pred. No. 6.6e-102; Matches 217; Conservative 31; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/07/704,288C
22-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8899
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/07704288C Patent No. 5399680 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LAMB, CHRISTOPHER J. APPLICANT: ZHU, QUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: P:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 444 SOLL...
CITY: LOS Angeles
STATE: California
COUNTRY: United States
7 TP: 90071-2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
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MOLECULE TYPE: protein
US-07-704-288C-8
                                                                                                                                                                                                                                                                                                                                                                                             305 SYGDNLDCYNQRPF 318
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US-07-704-288C-8
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      68 GPGPGPV-TGGDLGSVISNSMFDQMLKHRNENSCQGKNNFISYNAFITAARSFPGFGTSG 126
                                                                                          185 KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS 244
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                                                                 STDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPG 184
                                                                                                                                                                                                                                 245 HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV 304
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                                                                                                                                                                        Indels 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500,1800 Diagonal
STREET: Road, PO Box 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.1%; Score 1202.5; DB 2
67.8%; Pred. No. 5.9e-102;
iive 38; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/842,165
FILING DATE: 19920501
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/348
TELECOMMUNICATION INFORMATION:
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APPLICAMY: LEGUAY, Jean-Jacques
APPLICAMY: PIGNARD, Annie
APPLICAMY: PIGNARD, Annie
TITLE OF INVENTION: Recombinant ge
TITLE OF INVENTION: having endochi
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Patent No. 5932699
GENERAL INFORMATION:
APPLICANT: DUBOIS, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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(703) 683-4109
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AMINO ACID
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Best Local Similarity 67.8's
Matches 213; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                        307 SPGDNLDCGNQRSF 320
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US-07-842-165-13
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STATE:
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Matches 217;
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                                                                                      TGSTDVKKREVAAFLAQISHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCA 182
                             63 SGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFAT 122
                                                                                                                                                 PCKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKP
                                                                                                                                                                10 VAYLLFSLLVLVESAALAQNCGSQGGGKACASGQCCSKFGWCGNTNDYCGSGNCQSQ---C
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APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: LAMB, CHRISTOPHER J.
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08379259
Patent No. 5695939
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 330 amino acids
amino acid
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                                                                                                                                                                                                                                                                     303 GVSYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: protein
US-08-379-259-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United State ZIP: 90071-2921 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
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                                                                                                                                                                            SEDINARKREIAAFFAQTSHETTGGWASAPDGPYAWGYCFLRERGNPGDYCPPSSQWPCA 183
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                                                                                                244 SCHDVIIGRMNPSSADRAANRLPGFGVIINIINGGLECGRGTDNRVQDRIGFYRRYCSIL 303
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                                                                         SGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFAT 122
                                                                                                                                                       123 IGSTDVKKREVAAFLAQISHETIGGWPTAPDGPYSWGYCFNQERGAISDYCIPSSQWPCA 182
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                                   10 VAYLLESLLVLVSAALAQNCGSQGGGKACASGQCCSKFGWCGNTNDYCGSGNCQSQ---C 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALMFWMTPQSPKP
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7 VAMLAAAFAV---SAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGC
                                                                                                                                                                                                                                     PGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKP
                                                                                                                                                                                                                                                                                                                   SSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.0%; Score 1183; DB 4;
67.1%; Pred. No. 3.5e-100;
Live 36; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCORDATION:
APPLICANT: RAIKhel, Natasha V.
TITLE OF INVENTION: Nettle Lectin cDNA
FILE REFERENCE: MSU 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-791-931-7; Sequence 7, Application US/07791931C; Patent No. 6133507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Phaseolus vulgaris
US-07-791-931-7
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4

Length 330

Score 1202; DB 1; Pred. No. 6.6e-102;

68.1**%**; 68.7**%**;

Query Match Best Local Similarity

Search completed: May 3, 2002, 18:43:05 Job time: 748 sec

us-09-534-229c-3.rai

Page 9

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May 3, 2002, 18:32:12; Search time 88.01 Seconds (without alignments) 276:101 Million cell updates/sec
                                                                                                                                                                                          US-09-534-229C-3
1765
1 MRGVVVVAMLAAAFAVSAHA......DLLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                                                                                                  219241
GenCore version 4.5 copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                        219241 seqs, 76174552 residues
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                      Run on:
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C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;21-62/Domain: hevein chitin-binding domain homology <hcb> F;82-320/Domain: plant chitinase homology <pch></pch></hcb>
Query Match 96.1%; Score 1696.5; DB 2; Length 320; Best Local Similarity 95.3%; Pred. No. 6.8e-119; Matches 305; Conservative 9; Mismatches 5; Indels 1; Gaps 1;
QY 1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
Db 1 MRGVVVVAMLABABRAVSAHABQCGSQAGGATCPNCLCCSKFGFCGSTSDYCGNGCQSQCN 60
Qy 61 GCS-GGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSG 119
DD 61 GCSGGGTPVPVPTPTGGGVSSIISQSLFDQMLLHRNDAACQAKGFYNYGAFVAAANSFSG 120
OY 120 FATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQW 179
Db 121 FATTGGADVRKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAASDYCSPNSQW 180
OY 180 PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDELNNPDLVASDATVSFKTALWFWMTPQS 239
Db 181 PCAPGKXYFGRGPIQISYNYNYGPAGRAIGTDLLNNPDLVATDATVSFKTALMFWMTPQS 240
Oy 240 PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 299
Db 241 PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 300
QY 300 DILGVSYGDNIDCYNQRPFA 319
Db 301 DILGVIYGDNLDCXNQRPFA 320
RESULT 2

JC2071 chitinase (EC 3.2.1.14) a - rye

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Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; Keywords: glycosidase; hydrolase; lectronain: hevein chitin-binding domain homology <HCB>;21-62/Domain: hevein chitin-binding domain homology <PCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUADOLA
Chitinase (EC 3.2.1.14) - rice
NiAlternate names: endochitinase
Chitinase (EC 3.2.1.14) - rice
NiAlternate names: endochitinase
C; Species: Oryza sativa (rice)
C; Species: Oryza sativa (rice)
C; Accession: 103614
R; Mishizawa, Y:, Kishimoto, N:, Saito, A.; Hibi, T.
R; Mishizawa, Y:, Kishimoto, N:, Saito, A.; Hibi, T.
Mol. Gen. Genet. 24. 1-10, 1993
A; Mitle: Sequence variation, differential expression and chromosomal location of A; Reference number: S39979; MUID:94049667
A; Recession: 103614
A; Residues: Urge: DNA
A; Residues: 1-323 <NIS>
A; Molecule type: DNA
A; Residues: 1-323 <NIS>
A; Molecule type: Lory
A; Molecule type: Lory
A; Molecule type: DNA
A; Residues: 1-323 <NIS>
A; Genetics:
A; Genetics:
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homo C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology <HCB>
F; 82-627Domain: plant chitinase homology <PCH>
F; 82-322/Domain: plant chitinase homology <PCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAT--SDYCT
                                                                                                                                                                                                                                                            PCAPGKKYFGRGP1Q1SHNYNYGPAGQA1GTDLLNNPDLVASDATVSFKTALMFWMTPQS
                                                                                                                                                                                                                                                                                                                                                                           FATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQW
                                                                                                                                                                                                  240 PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC
                         GCSGGTPVPVPTPS-GGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSG
MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN
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299 DILGVGYGNNLDCYSQRPFA 318
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A; Experimental source: cv. NK1558
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; C; Superfamily: lectin-related plant chitinase; polysaccharide degradation
F;1-19/Domain: signal sequence *status predicted < CMAT>
F;20-318/Product: chtinase *status predicted < CMAT>
F;20-60/Domain: hevein chitin-binding domain homology <HCB>
F;80-318/Domain: plant chitinase homology <PCH>
                C;Species: Secale cereale (rye)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999
C;Accession: JC2071
B;Yamaqami, T.; Funatsu, G.
Biosci, Biotechnol. Biochem. 58, 322-329, 1994
A;Title: The complete amino acid sequence of chitinase-a from the seeds of rye (Secale A;Tieference number: JC2071; MUID:94169514
A;Accession: JC2071
A;Accession: JC2071
A;Residues: 1-302 < YAM>
C;Superfamily: lectin-related plant chitinase; hevein chittin-binding domain homology; C;Reywords: 91ycosaidase; polysaccharide degradation
F;1-42/Domain: hevein chitinase homology <PCH>
F;64-302/Domain: plant chitinase homology <PCH>
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R) Ignatius, S.M.J.; Huang, J.; Muthukrishnan, S.
R) Ignatius, S.M.J.; Huang, J.; Muthukrishnan, S.
Submitted to the EMBL Data Library, September 1993
A; Description: Isolation and characterization of a barley chitinase genomic A; Reference number: 215336
A; Accession: T04403
A; Accession: T04403
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Miller Lype; DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable chitinase (EC 3.2.1.14) precursor - barley
C;Species: Hordeum vilgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHDVITGRWSPSGA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSYGDNLDCYNQRP 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGSTDVKKREVAAFL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09
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77.8%; Pred. No. 2e-97;
                                                                                                                                                                                                                                                                                                                                                                      80.3%; Score 1416.5; Dl
82.1%; Pred. No. 4e-98;
iive 26; Mismatches
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Best Local Similarity 82.1%
Matches 248; Conservative
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Best Local Similarity
Matches 249; Conserv
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FA 302
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δ qq δà g ŏ g rice

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C; Species: Organ sativa (rice)
C; Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C; Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C; Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C; Ruu, O: Lamb, C.J.
Mol. Gen. Genet. 226, 289-296, 1991
A; The first speciation and characterization of a rice gene encoding a basic chitinase.
A; Reference number: 315997; MUID: 91238706
A; Reference number: 315997
A; Reference number: 3159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 N-----GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTAL 231
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                                                                                                                                                                                                                                                                                                                                                                                                                       STDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTETRKREVAAFLGQTSHETTGGWPTAPDGPFSWGYCFKQEQNPPSDYCQPSPEWPCAPG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS 244
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                                                                                                                                                                                                                                                                                                         GTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTG 124
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                                                                                                                                                                                                                           VVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGCSG
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                                                                                                                                  2;
                                                                                Length 339;
                                                                                                                                     47; Indels
                                                                                Score 1313; DB 2;
Pred. No. 2.2e-90;
                                                                                                                                     36; Mismatches
F;91-329/Domain: plant chitinase homology <PCH>
                                                                                   74.48;
72.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S15997
chitinase (EC 3.2.1.14) - rice
                                                                                      Query Match 74.49
Best Local Similarity 72.99
Matches 229; Conservative
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A; Residues: 1-339 <NIS>
A; Cross-references: EMBL:X56787
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
E; 33-74/Domain: hevein chitin-binding domain homology <HCB>
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C;Species: Oryza sativa (rice)
C;Date: 18-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C;Datession: S39979
C;Accession: S39979
A;Rishiawa, Y.;Kishimoto, N.; Saito, A.; Hibi, T.
Mol. Gen. Genet. 241, 1-10, 1993
A;Ritle: Sequence variation, differential expression and chromosomal location of rice A;Reference number: S39979; MUID:94049667
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                               A) Reference number: $40414
A) Accession: $40414
A) Accession: $40414
A) Accession: $40414
A) Molecule type: mRNA
A) Residues: 1-340
A) Coss-references: EMBL:X56787; NID:g407471; PIDN:CAA40107.1; PID:g407472
A) Cross-references: EMBL:X56787; NID:g407471; PIDN:CAA40107.1; PID:g407472
C) Superfamily: lectin-related plant chitinase; polysccharide degradation
F) 33-74/Domain: hevein chitin-binding domain homology <HCE>
F) 92-330/Domain: plant chitinase homology <PCH>
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C;Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
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Pred. No. 1e-90;
5; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, November 1990
                                                                    298 YKRYCDMLGVSYGANLDCYNQRPF 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
74.6%; Sco
Best Local Similarity 72.4%; Pro
Matches 228; Conservative 36;
                                         295 YKRYCDLLGVSYGDNLDCYNQRPF
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                                                                                                                                                                                                                                       chitinase (EC 3.2.1.14)
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R; Nishizawa, Y.
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domain homology;

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A; Molecule type: DNA kesidue. 1-318 < HUA> kesidue. 1-318 < HUA> kesidue. 1-318 < HUA> kyesidue. 1-318 < HUA> kyesidue. 1-318 < HUA> kyesidue. 1-318 < HUA> kyesidue. 1-319 < HUA-154367; NID:920195; PIDN:CAA38249.1; PID:920196 C; Superfamily: lectin-related plant chitinase; hevein chitin-binding dome C; Keywords: glycosidase, hydrolase; polyaccharide degradation F; 19-60/Domain: hevein chitin-binding domain homology < HCB> F; 79-316/Domain: plant chitinase homology < PCH>
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Best Local 3
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Matches
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Filed, R.; Skriver.
Filed, S.; Striver.
Filed, R.; Skriver.
Filed
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A; Title: Nucleotide sequence of a rice genomic clone that encodes a class I endochitinas A; Reference number: S14948; MUID:91370895
A; Accession: S14948
A; Status: preliminary
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C;Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: S14948
                                                                                                                                                                                                                                                                                               probable chitinase (EC 3.2.1.14) - barley
C;Species: Hordeum vulgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCQSQCNGCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRN----DAACLAKGFYNYGAF 110
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                              292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRG------VVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGT
      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 8.4e-89;
33; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1291.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIGEYKRYCDLLGVSYGDNLDCYNQRPF 318
                                                                                         IGFYKRYCDLLGVSYGDNLDCYNQRPFA 319
                                                                                                                              chitinase (EC 3.2.1.14) - rice
N;Alternate names: class I endochitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.2%;
71.6%;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chitinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Subside (EC 3.2.1.14) precursor - common tobacco chitinase (EC 3.2.1.14) precursor - common tobacco chitinase (EC 3.2.1.14) precursor - common tobacco) C.Species: Nicotiana tabacum (common tobacco) C.Species: Nicotiana tabacum (common tobacco) C.Species: Nicotiana tabacum (common tobacco) C.Species: Nicotians 1993 #sequence_revision 29-Jan-1993 #text_change 22-Jun-1999 C.Spacesion: S08627; J000993 T.Spin 14, 357-368, 1990 T.Spin 15.0. T.Spin 16. Structure of a tobacco endochitinase gene: evidence that different chitis A; Reference number: S08627 MCID:91346623 A; Reference number: S08627 MCID:91346623 A; McIccule type: DNA A; Residues: 1-329 cSHI> A; Residues: 1-329 cSHI> A; Residues: 1-329 cSHI> A; Residues: DNA A; Residues: DNA A; Residues: DNA A; Residues: DNA A; Reference number: J00993; MCID:92404740 A; Title: Chitinase, beta-1, 3-qlucanase, osmotin, and extensin are expressed in to A; Reference number: J00993; MCID:92404740 A; Residues: 1-72, H; J4, 74, 7FRC', 79-262, S', 264-329 cNEA> A; Cross-references: GB:S44869; NID:9256132; PIDN:AAB23374.1; PID:9256133 A; Cross-references: GB:S44869; NID:9256132; PIDN:AAB23374.1; PID:9256133 A; Cross-references: CB:S44869; NID:926132; PIDN:AAB23374.1; PID:9256133 A; Cross-references: CB:S44869; NID:9266132; PIDN:AAB23374.1; PID:9256133 A; Cross-references: Lhin cell layer, cv. samsun nn C; Comment: This protein is expressed mainly in roots. C; Genetics: A; Thirpos: 14841, 1997.
                                                                          4;
                                                                                                                                                                                                                                                                             61 GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGF 120
                                                                                                                                                                                                                                                                                                                         PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 299
                                                                          Gaps
                                                                                                                                          9
                                                                                                                                      1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQE-RGATSDYCTPSSQW
                                                                       5
Length 318;
                                                                          Indels
   DB 2;
                                                                          26;
   Score 1289.5; DB Pred, No. 1.1e-88;
                                                                              24; Mismatches
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C.Species: Orgas sativa (fice)
C.Species: Orgas sativa (fice)
C.Species: Orgas sativa (fice)
C.Species: Orgas sativa (fice)
C.Species: Orgas sativa
C.Species: J6-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C.Species: J6-Septem (J6-Septem)
R.Kim, Y.K.; Back, J.M.; Park, H.Y.; Choi, Y.D.; Kim, S.I.
Biosci. Biotechnol. Biochem. 58, 1164-1166, 1994
A.Fitle: Isolation and characterization of CDNA clones encoding class I chitinase in A.Fretene number: JC2252; MUID:94319069
A.Fretenene number: JC2252
A.Molecule type: mRNA
A.Residues: 1-319 extinA
A.Residues: In319 extinA
A.Residues: This enzyme catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-C.Comment: This enzyme catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-C.Comment: This enzyme catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-C.Comment: Signal Sequence #status predicted degradation
F.1-20/Domain: signal Sequence #status predicted <AMT>
F.21-319/Product: chitinase class I, CHI6 #status predicted <AMT>
F.21-62/Domain: hevein chitinase homology <PCH>
F.21-62/Domain: plant chitinase homology <PCH
F.21-62/Domain: plant chitinase homology <PCH
F.21-62/Domain: plant chitinase plant chitinase homology <PCH
F.21-62/Domain: plant chitinase plant chitinase plant chitinase pl
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N;Alternate names: CHN50 protein; endochitinase
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 22-Jun-1999
C;Accession: S20981; A29074; S13322; S19855
R;van Buuren, M.; Neuhaus, J.M.; Shinshi, H.; Ryals, J.; Meins Jr., F.
Mol. Gen. Genet. 232, 460-469, 1992
A;Title: The structure and regulation of homeologous tobacco endochitinase 9
A;Reference number: S20981; MUID:92269767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCSGGTPVPVPTPSGG--GVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 GEATTGSIDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAT--SDYCTPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN
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                                                                                                                                                                                                                                                                                         chitinase (EC 3.2.1.14) class I, CH16 precursor
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                                                                   DRIGEYKRYCDLLGVSYGDNLDCYNQRPF
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Matches 235; Conservative
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Best Local Similarity
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S54806
Chitinase (EC 3.2.1.14) class I precursor - rice
chitinase (EC 3.2.1.14) class I precursor - rice
(S.Specides: Oryza sativa (rice)
C.Specides: Oryza sativa (rice)
C.Date: O8-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 22-Jun-1999
C.Date: O8-Jul-1996
R.W. Y.; Zhu, O.; Panbangred, W.; Shirasu, K.; Lamb, C.
Plant Mol. Biol. 30, 387-401, 1996
A.; Reference number: S65771; MUID:96189256
A.; Reference number: S65771
A.; Reference number: S65771
A.; Reference number: S65772
A.; Reference number: S65771
A.; Residues: 17-32 < xuz.>
A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EWBL:X87109; NID:q807954; PIDN:CAA60590.1; PID:q807955 C; Superfamily: lectin-related plant chitinase; hevein chitin binding domain C; Keywords: glycosidase; hydrolase; polysaccharide degradation F: 21-62/Domain: hevein chitin-binding domain homology <HCB> F: 82-321/Domain: plant chitin-benouogy <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 ALWEWMTPQSPKPSSHDVIJGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 AFWEWMIPQSPKPSCHAVMIGOWIPNGNDQAAGRVPGYGVTVIINGGVECGHGADSRVA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 AAANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAT-- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----NGCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFV 111
                                                                                                                                                                                                                                                                                                                                             TDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSH 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                     PVPVPTPSGGG-VSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC- 59
                                                                                                                                                  99
                                                                                                                                                                                                                          68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AAANAFPTFATTGDAATRKREVAAFLAQTSHETMGGWATAPDGPYSWGYCFKEENNGNVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDYCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
                                                                                                                                                                                                                              SLLFSLLLLSASAEQCGSQAGGARCPSGLCCSKFGWCGNTNDYCGPGNCQSQCPG--GPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
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   Length 329,
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                                                                           Indels
   .;
                                                                           50;
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   DB
                                       4.6e-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28; Mismatches
Score 1281.5;
Pred. No. 4.6e
                                                                           29; Mismatches
Query Match
Best Local Similarity 73.2%;
Matches 229; Conservative 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 PGDNLDCGNQRSF 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 YGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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chitinase (EC 3.2.1.14) class I precursor (clone ChtB3) - potato (fragment)
N;Alternate names: basic chitinase precursor
C;Species: Solanum tubercosum (potato)
C;Species: 20-ort-1994 #sequence_revision 01-Sep-1995 #text_change 22-Jun-1999
C;Accession: 543317; S06161
R;Beerhues, L.; Kombrink, E.
Piant Mol. Biol. 24, 353-367, 1994
A;Title: Primary structure and expression of mRNAs encoding basic chitinase and 1,3-b
A;Reference number: 543317; MUID:94154255
A;Accession: 843317
A;Molecule type: mRNA
A;Residues: 1-318 <BEE>
A;Cross-references: EMBE: U02607; NID:9467823; PIDN:AAA17409.1; PID:9467824
R;Laflamme, D.; Roxby, R.
Plant Mol. Biol. 13, 249-250, 1989
A;Title: Isolation and nucleotide sequence of cDNA clones encoding potato chitinase g
A;Reference number: S06161; MuID:92003671
A;Accession: S06161
A;Reference number: EMBE:X14133; NID:921465; A;Cross-references: EMBE:X14133; NID:921464; PIDN:CAA32351.1; PID:921465
A;Cross-references: EMBE:X14133; NID:921464; PIDN:CAA32351.1; PID:921465
A;Note: the authors translated the codon CAG for residues 54 and 303 as Gly, YGC for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of mRNAs encoding basic chitinase and 1,3-b
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A;Cross-references: EMBL:U02605; NID:9467819; PIDN:AAA18332.1; PID:9467820 C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain C;Keywords: glycosidase; hydrolase [F:19-61/Domain: hevein chitin-binding domain homology <HCB> F:19-10/Domain: plant chitin-binding domain homology <HCB> F:71-310/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                            61 --GPGPSGDLGGV---ISNSWFDQMLNHRNDNACQGKGNFYSYNAFISAAGSFPGFGTTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                               68 VPVPTPSG--GGVSSIISQSLFDQMLLHRNDAACLAKG-FYNYGAFVAAANSFSGFATTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 STDVKKREVAAFLAQTSHETIGGWPTAPDGPYSWGYCFNQERGAISDYCTPSSQWPCAPG 184
                                                                                                                                                                                                                                                                                                                                 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS
                                                                                                                                                                                                                                                                                  9 MLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <PRO>
                                                                                                                                                                                                                                                                                                            y C. Superfamily: lectin-related plant chitinase; hevein chitin-binding converges glycosidase; hydrolase; polysaccharide degradation converges a signal sequence (fragment) #status predicted <SIG> F:10-18/Domain: chitinase #status predicted <MAI> F:19-61/Domain: hevein chitin-binding domain homology <HCB> F:17-310/Domain: plant chitinase homology <PCH> F:71-310/Domain: carboxyl-terminal propeptide #status predicted <PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
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                                                                                                                                                                               318;
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                                                                                                                                                                               Length
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                                                                                                                                                                               DB 2;
                                                                                                                                                                            71.1%; Score 1255.5; DB 2;
llarity 72.6%; Pred. No. 3.8e-86;
Conservative 26; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.8%; Score 1250.5; DB 371.6%; Pred. No. 8.9e-86; ive 29; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 227; Conservative
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Best Local Similarity
                                                                                                                                                                                                            Local Similarity
es 228; Conserv
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                  Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                         a tobacco endochitinase gene in suspension-cul
                                                                                                                                       chitinase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Superfamily: lectin related plant chitinase; hevein chitin-binding domain homology; C; Keywords: glycosidase; hydrolase; polysaccharide degradation F;1-23/Domain: signal sequence #status predicted <SIG>F;24-324/Product: chitinase # #status predicted <MAI>F;24-66/Domain: hevein chitin-binding domain homology <HCB>F;78-316/Domain: plant chitinase homology <PCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 VIIGRWQPSSADRAANRLPGFGVITNINGGLECGRGTDSRVQDRIGFYRRYCSILGVSP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMLABARAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SILFSILLISASAEQCGSQAGGARCASGLCCSKFGWCGNTNDYCGPGNCQSQCPG--GPT-68
                                                                                                                                       inhibition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL:X51599; NID:g19844; PIDN:CAA35945.1; PID:g19845
                                       PID:919847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TARKREIAAFFAQTSHETTGGWATAPDGPYAWGYCWLREQGSPGDYCTPSGQWPCAPGRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chitinase (EC 3.2.1.14) precursor (clone ChtB1) - potato (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                     A; Cross-references: EMBL:X64519; NID:g19846; PIDN:CAA45822.1;
                                                                                                                                             enzyme:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.4%; Score 1261; DB 2;
72.1%; Pred. No. 1.5e-86;
tive 29; Mismatches 50;
                                                             A; Experimental source: cv. Havana 425.
Kshinshi, H.; Mohem, D.; Melns Jr., F.
Proc. Matl. Acad. Sci. U.S.A. 84, 89-93, 1987
A; Title: Regulation of a plant pathogenesis-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Solanum tuberosum (potato)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of mRNAs
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Plant Mol. Biol. 24, 353-367, 1994
A;Title: Primary structure and expression of
A;Reference number: S43317; MUID:94154255
A;Accession: 565019
A;Status: preliminary; translation not shown
A;Residues: 1-318 <BEE>
                                                                                                                                                                                                                                                                                                                                            A,Title: Gene structure and expression of A,Reference number: S13322; MUID:91363829
                                                                                                                                                                                                                                       A;Molecule type: mRNÅ
A;Residues: 15-324 <SHI>
R;Fukuda, Y:; Ohme, M:; Shinshi,
Plant Mol. Biol. 16, 1-10, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: cv. BY4
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                  A; Reference number: A29074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 225; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-324 <FUK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Introns: 143/1; 194/2
                                                                                                                                                                                                               A; Status: preliminary
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                                                                                                                                                                                            A; Accession: A29074
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5,

Search completed: May 3, 2002, 18:32:13 Job time: 7476 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:48:32; Search time 78.59 Seconds (without alignments) 148.824 Million cell updates/sec

Title: US-09-534-229C-3
Perfect score: 1765
Sequence: 1 MRGVVVVAMLAAAFAVSAHA.....DLLGVSYGDNLDCYNQRPFA 319

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 100059 seqs, 36664827 residues

Notal number of hits satisfying chosen parameters: 1000059

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

IES	Descripti	PI1955 hordew	P25765 oryza sa	P24626	P08252	P24091 nicotian	P52403 solanum	. P52405 solanum	Q05538 lycopers	P52404 solanu	pisum		P05315	n P29059 n	P52406	009023	P19171		r P06215	039799	r P36361	039785	Q41596 theobrom	P23951 hordeum	P16579 populus	Q05537 lycopers	P29031 populus	P29021 petunia	P16061 populus	Q05540 ly	P17514 r	P17513 nicotian	P11218 urtica di	<u></u>
SUMMARIES	Ω	HORV	CHI2_ORYSA	CHI1_ORYSA		CHI2_TOBAC	CHII_SOLTU	CHI3_SOLTU	CHIC LYCES	CHI2_SOLTU	CHIX_PEA	CHI2_PEA	CHIT_SOLTU	CHI3_TOBAC	CHI4_SOLTU	CHI2_BRANA	CHIT_ARATH	CHIB_VITVI	CHIT_PHAVU	CHI1_GOSHI	CHI5_PHAVU	CHI2_GOSHI	CHI1_THECC	CHI2_HORVU	CHI6_POPTR	CHID_LYCES	CHIB_POPTR	CHIT_PETHY	CHI8_POPTR	CHIB_LYCES	CHIQ_TOBAC	CHIP_TOBAC	AGI_URTDI	CHIA LYCCI
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d	s uery atch	7.67	73.7	73.1	72.6	71.4	71.1	70.8	70.7	70.3	68.8	68.4	68.4	68.3	67.6	67.6	67.5	67.3	67.0	9.99	66.2	65.4	65.2	63.7	57.9	56.9	49.5	45.6	45.5	44.8	44.5		40.9	
	Score	1407.5	1301.5	1289.5	1281.5	1261	1255.5	1250.5	1248.5	1240.5	1215	1208	1208	1206	1193.5	1192.5	1190.5	1187.5	1183	1178.5	1168.5	1154.5	1151.5	1125	1022.5	1004	874.5	805.5	803.5	791.5	785.5	763.5	722.5	712.5
	u.j.	7	7	m	₹	Ŋ	9	7	80	Q	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	23

Q05539 lycopersico	P42820 Deta Vulgar	P29023 zea mays (m	Q06209 brassica na	P29022 zea mays (m	P27054 phaseolus v	P80052 dioscorea j	P29032 populus tri	P15326 coix lachry	Q06015 arachis hyp	P15312 hordeum vul	Q06012 arachis hyp	
CHIA_LYCES	CHIP_BETVU	CHIB_MAIZE	CHI4_BRANA	CHIA_MAIZE	CHI4_PHAVU	CHIT_DIOJA	CHIC_POPTR	IAMY_COILA	CHI3_ARAHY	AGI_HORVU	CHIA_ARAHY	
Н	H	Н	Н	Н	Н	7	Н	П	Н	Н	H	
253	288	269	268	280	270	250	121	133	46	212	46	
39.2	34.5	34.0	32.8	32.7	31.0	28.5	16.8	16.2	11.8	11.6	11.4	
692.5	609.5	599.5	579	577	547	503	297	285.5	208	205	201	
34	35	36	37	38	30	4	4.	42	-4	44	45	

ALIGNMENTS

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                                                               First. 12, Created)
01-0CT-1989 (Rel. 12, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOT-1997 (Rel. 35, Last annotation update)
101-NOT-1997 (Rel. 35, Last annotation update)
Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. HIMALAYA;
Swegle M., Huang J.-K., Lee G., Muthukrishnan S.;
"Identification of an endochitinase cDNA clone from barley aleurone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- CATALYTIC ACTIVITY: HYDROIXSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-:- INDUCTION: BY ETHYLENE.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Mol. Biol. 12:403-412(1989).
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-CV. NK 1558; TISSUE-Leaf; Ignatius S.M.J., Huang J., Muthukrishnan S.; Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                               318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P23951, 2BAA.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; I.
Pfam; PF00182; Glyco_hydro_19; I.
PRINIS; PR00451; CHITINBINDNG.
ProDom; PD000574; Glyco_hydro_19; I.
ProDom; PD000509; Chitin_bind; I.
SMART; SM00270; Chitbil; I.
PROSITE; PS00773; CHITINASE_19_1; I.
                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- FUNCTION: THIS PROTEIN FUNCT
CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 141-318 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U02287; AAA18586.1; -. EMBL; X15349; CAA33407.1; -.
                                 STANDARD;
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                                                                                                                                                                                                     Triticeae; Horde
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYDROLASES)
                             CHI1_HORVU P11955;
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             CHI1_HORVU
RESULT
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DOMAIN
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                                                                                                                                                                                                          120 FATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQW 179
                                                                                                                                                         1 MRGVVVVAMIAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC STATUTING THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHIIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
Bukaryota, Vitidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
CHITINASE_19_2; 1.
dase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                               61 GCSGGTPVPVPTPS-GGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSG
                                                                                                                                                                                                                                                                         PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS
                                                                                                                                                                                                                                                                                    Gen. Genet. 226:289-296(1991).
FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91238706; PubMed=2034221; Zhu Q., Lamb C.J.; "Isolation and characterization of a rice gene encoding a basic chitinase.";
                                                                                                                                         ω
.,
                                                                                                                     Length 318;
                          POTENTIAL.
26 KDA ENDOCHITINASE 1.
26 KDA ENDOCHITINASE 1.
CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W, 42D62B2FE8041954 CRC64;
                                                                                                                                         Indels
                                                                                                                       DB 1;
                                                                                                                                         35;
                                                                                                                      79.7%; Score 1407.5; DB 77.8%; Pred. No. 8.1e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
BAIST ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14)
RCH10.
                                                                                                                                                                                                                                                                                                                                                                                                                   336 AA
                                                                                                                                         33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                   DLLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                                                                                              MM:
                           318
62
37
43
49
57
33402 1
                                                                                                                       Query Match
Best Local Similarity 77.8
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
 PS00774; CHITIN
e; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S15997; S15997.
HSSP; P23951; 2BAA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4530;
          Hydrolase; Glyco:
Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                    CHI2_ORYSA
P25765;
                                              DOMAIN
DISULFID
DISULFID
                                                                          DISULFID
                                                                                              SEQUENCE
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CHI2_ORYSA
                              SIGNAL
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                                       CHAIN
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InterPro; IPR001002; Chitin_bind.

R InterPro; IPR001002; Glyco_hydro_19.

R Ffam; PP00187; chitin_binding; 1.

R Ffam; PP00187; chitin_binding; 1.

R FTNTS; PR00451; CHTTINBINDO.

R PRODOM; PD0000679; CHITINBINDO.

R PRODOM; P0000679; CHITIN_bind; 1.

R RANRY; SW00270; CHITIN_bind; 1.

R ROSITE; PS00773; CHITINASE_19.; 1.

R PROSITE; PS00774; CHITINASE_19.; 1.

R PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. JAPONICA; TISSUE-Seedling;
MEDLINE=91370895; PubMed=1893114;
Huang J.K., Wen L., Swegle M., Tran H.C., Thin T.H., Naylor H.M.,
Muthukrishnan S., Reeck G.R.;
"Nucleotide sequence of a rice genomic clone that encodes a class I endochitinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
cnarmatonhvta; Magnoliophyta; Lillopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRGVVVVAMLAAAF-AVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASIC ENDOCHITINASE 2.
CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Indels
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7F4EC126265DEA84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6e-91;
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01-MAR-1992 (Rel. 21, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
BASIC ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 IGFYKRYCDILGVSYGANLDCYSQRPSA 320
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Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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334
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RESULT 4
CHI1_TOBAC
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                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQE-RGATSDYCTPSSQW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 ATTRDADTCKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFKEENNGNAPTYCEPKPEW 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycosidase; Chitin degradation; Chitin-binding; Signal;
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                                                         N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LEGITIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
Plant Mol. Biol. 16:479-480(1991).
-!- FUNCATION: THIS PROFIEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
-!- CATALITIC ACTIVITY: HYDROLISIS OF THE 1,4-BETA-LINKAGES OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.1%; Score 1289.5; DB 1; Length 318; 73.4%; Pred. No. 5.7e-90; tive 24; Mismatches 56; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASIC ENDOCHITINASE 1.
CHITIN-BINDING (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                       Interpro: IPR001002; Chitin_bind.
InterPro: IPR00726; Glyco_hydro_19.
Pfam: PF00187; chitin_binding; 1.
Pfam: PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
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318
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                                                                                                                         HYDROLASES).
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Multigene fa
SIGNAL
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Best Local 3
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                                                                                                                                                                                                                                                                                                                      Shinshi H., Neuhaus J.-M., Ryals J., Meins F. Jr., Structure of a tobacco endochitinase gene: evidence that different chitinase genes can arise by transposition of sequences encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
-!- INDUCTION: BY ETHYLENE.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotlana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               containing proteins.";
Science 257:655-657(1992).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
--- CONTAINING FUNAL PATHOGENS.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION.
MEDLINE-92052270; PubMed-1946457;
Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.;
Neuhaus J.M., Sticher L., Meins P. Jr., Boller T.;
A short C-terminal sequence is necessary and sufficient for the targeting of chitinases to the plant vacuole.";
Proc. Natl. Acad. Sci. U.S.A. 88:10362-10366(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sticher L., Hofsteenge J., Milani A., Neuhaus J.M., Meins F. Jr
"Vacuolar chitinases of tobacco: a new class of hydroxyproline-
                                    01-AUG-1988 (Rel. 08, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-AUG-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE A PRECURSOR (EC 3.2.1.14) (CHN-A).
  329 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X16939; CAA34813.1; -. PTR; S08627; S08627. HSSP; P29351; 2BAA.
INTERPLO; IPR001002; Chitin_bind.
InterPro; IPR00726; Glyco_hydro_19.
Pfan; PF00187; chitin_binding; 1.
Pfan; PF00182; Glyco_hydro_19; PRNNTS; PR00451; CHITINBINDNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000574; Glyco_hydro_19; 1. ProDom; PD000609; Chitin_bind; 1.
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                                                                                                                                                                                                                                                                                      STRAIN-CV. HAVANA 425; TISSUE-Leaf;
MEDLINE-91346623; PubMed-1966383;
                                                                                                                                             Nicotiana tabacum (Common tobacco).
                                                                                                                                                                                                                                                                                                                                                                                                          Plant Mol. Biol. 14:357-368(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92358209; PubMed=1496378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydroxylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X16938; CAA34812.1; -.
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00270; ChtBD1;
                                                                                                                                                                                                                                                                                                                                                                                         cysteine-rich domain.";
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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CHI1_TOBAC
P08252;
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                                                                                                                                                                                                                                                                                                                                                                                                           TDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYFGRGPIQISHNYNGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSH 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 DYITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVS 305
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STRAIN-CV. HAVADMA 425; TISSUE-Leaf;
MEDLINE-92269767; Pubmed-1588915;
van Buuren M., Neuhaus J.-M., Shinshi H., Ryals J., Meins F. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression of a tobacco endochitinase gene in tobacco cells.";
                                                                                                                                                                                                                                                                                                                                                 8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
                                                                                                                                                                                                                                                                                              'n
                                     CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
                                                                                                                                                                                                                                                             Length 329;
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3EC99D96E6C0114C CRC64
                           REMOVED IN MATURE FORM
                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE B PRECURSOR (EC 3.2.1.14) (CHN-B).
                                                                                                                                                                                                                                                               Score 1281.5; DB Pred. No. 2.4e-89;
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                                                                                                                                                                                                                                                                                              29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CV. BRIGHT YELLOW 4; TISSUE=Leaf;
MEDLINE=919503829; Pubmed=1888899;
Fukuda Y., Ohme M., Shinshi H.;
"Gene structure and expression of a tobac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Mol. Biol. 16:1-10(1991).
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73.2%;
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329 AA;
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Best Local Similarity
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P24091;
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PIR; A29074; A29074.

PIR; S13322; S1332.

PIR; S20981; S20981.

PIR; S20981; S20981.

R HSSP, P23951; 2BAA.

PIR; PRO01002; Chitin_bind.

Pfam; PF00187; Chitin_binding; 1.

PRINTS; PR00451; CHITINBINDNG.

ProDom; PD000659; Chitin_bind; 1.

PRODM; PD000659; Chitin_bind; 1.

PROSTE; PS00070; CHEBI, 1.

PROSTE; PS00070; CHITIN_BINDING; 1.

PROSTE; PS00773; CHITIN_BINDING; 1.

PROSTE; PS00774; CHITIN_BINDING; 1.

PROSTE; PS00774; CHITIN_BENDING; 1.

PROSTE; PS00774; CHITIN_BENDING; 1.

PROSTE; PS00773; CHITIN_BENDING; 1.
                                                                                                                                                                                            Shinshi H., Mohnen D., Meins F. Jr.; "Regulation of a plant pathogenesis-related enzyme: inhibition of chitinase and chitinase mRNA accumulation in cultured tobacco tissues
structure and regulation of homeologous tobacco endochitinases of Nicotiana sylvestris and N. tomentosiformis origin."; Gen. Genet. 232:460-469(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-:- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
-:- INDCTION: BY ETHYLENE.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE=22052270; PubMed-1946457; Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.; Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.; M. Short C-terminal sequence is necessary and sufficient for the targeting of chitinases to the plant vacuole."; Proc. Natl. Acad. Sci. U.S.A. 88:10362-10366(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         containing proteins.";
Science 257:655-657(1992).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REMOVED IN MATURE FORM (PROBABLE) CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sticher L., Hofsteenge J., Milani A., Neuhaus J.M., Meins F. Jr
"Vacuolar chitinases of tobacco: a new class of hydroxyproline-
                                                                                                           [3]
SEQUENCE OF 15-324 FROM N.A., AND SEQUENCE OF 24-53.
                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 84:89-93(1987).
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
HYDROXYLATION.
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MEDLINE-92358209; PubMed=1496378;
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                                                                                                                                                                                                                                                                                           by auxin and cytokinin.",
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317
417
41
41
63
                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION.
                                                                                                                                                                      STRAIN-CV. HAVANA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
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MOD_RES
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DISULFID
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
BUYELLOPHENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING. SHILARNITY: BELOGNGS TO CHIMINASE CLASS IS WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N'TERMINAL CHITIN'BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                      127 DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK 186
                                                                                                                                                                                                                                                      246
                                                                                                                                                                                                                                                                                                                                                             VITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
                                                                                                                                                                                                                                                                                                                                                                              67 PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                                                                Gaps
                                                                                                                   99
                                                                                                                                                 9
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                                                                                                                                      YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD
                                                                                                                                                                                                                                                                                                                    8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
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                                                        Length 324;
                                                                                        Indels
            34721 MW; FA65DC2113B33EB6 CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
                                                                                      50;
                                                       71.4%; Score 1261; DB 1;
72.1%; Pred. No. 8e-88;
tive 29; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 AA
HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. DATURA; TISSUE=Leaf;
MEDLINE=94154255; PubMed=8111037;
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                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                            307 GDNLDCYNORPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
              324 AA;
                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4113;
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 69
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                                                                                        Matches 225;
                                                            Query Match
               SEQUENCE
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                                                                                                                                                                                                             69
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GPGPSGDLGGV---ISNSWFDQMLNHRNDNACQGKGNFXSYNAFISAAGSFPGFGTTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 SIDVKKREVAAFLAQTSHETIGGWPTAPDGPYSWGYCFNQERGAISDYCTPSSQWPCAPG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SINGULAR STANDAR STAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 VPVPTPSG--GGVSSIISQSLFDQMLLHRNDAACLAKG-FYNYGAFVAAANSFSGFATTG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Solanum tuberosum (Potato).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV
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REMOVED IN MATURE FORM, VACUOLAR
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CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 3 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.1%; Score 1255.5; DE
72.6%; Pred. No. 2e-87;
:ive 26; Mismatches 4
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                                                                                                                                                                       InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00182; Glyco_hydro_19; 1.
ProDom; PP00182; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00774; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
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42
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BB BB
58
33813 MW;
                                                                                                                             EMBL; U02605; AAA18332.1;
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18
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318
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21
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54
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P52405;
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DISULFID
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Matches 22
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CHI3_SOLTU
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-CV. MONEYMAKER;
MEDLINE-94003061; PubMed-8400122;
                                                                                                                                                                                                                                                                                                                                                                                         322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P23951; ZBAA.
InterPro: IPR001002; Chitin_bind.
InterPro: IPR0010026; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; I.
Pfam; PF00182; Glyco_hydro_19; I.
Pfam; PF00182; Glyco_hydro_19; I.
PRINTS; PR00451; CHTINBIRDNG.
ProDom; PD000694; Glyco_hydro_19; I.
ProDom; P0000699; Chitin_bind; I.
SWART; SM00270; ChtBD1; I.
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydroxylation; Multigene family.
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                                                                                                                                                                                                                                         LGVSYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                             LGVSPGDNLDCGNORSF 309
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                       CHIC_LYCES
Q05538;
                                                                                                                                                                                                                                                                                                                                                                       CHIC LYCES
                                                                                                                                                                                                                                         302
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                                                                                                                                                                                                                                                           -:- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-:- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPIAST (BY SIMILARITY).
-:- DEVELOPMENTAR LOCATION: VACUOLAR END PROTOPIAST (BY SIMILARITY).
-:- DEVELOPMENTAR LOCATION: LEAVES IN YOUNGER LEAVES OR STEMS SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                     OLD ROOT SEGMENTS, AND CARPELS.
INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING. SIMILARITY: BELONGS TO CHTINASE CLASS IS WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLIDE A N-TERMINAL CHIRN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 GTPVPVPTPSG--GGVSSIISQSLFDQMLLHRNDAACLAK-GFYNYGAFVAAANSFSGFA 121
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                                                                                                                                Beerhues L., Kombrink E.; "Primary structure and expression of mRNAs encoding basic chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                           and 1,3-beta-glucanase in potato.";
Plant Mol. Biol. 24:353-367(1994).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
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REMOVED IN MATURE FORM, VACUOLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TARGETING (POTENTIAL).
CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Indels
    euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY.
BF587A8515534E71 CRC64;
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; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
Probom; P0000574; Glyco_hydro_19; 1.
Probom; P0000609; Chitin_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PS00026; CHITIN BINDING; 1. PROSITE; PS00773; CHITINASE_19_1; 1. PROSITE; PS00774; CHITINASE_19_2; 1.
                                                                                                            MEDLINE=94154255; PubMed=8111037;
                                                                                                                                                                                                                                           CONTAINING FUNGAL PATHOGENS.
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SEQUENCE FROM N.A.
SMUDATN=CV. DATURA; TISSUE=Leaf;
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33798 MW;
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Best Local Similarity
Matches 227; Conserv
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                                                                                                                                                                                   242 PSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- CATALYTIC ACTIVITY: HYDROXYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-:- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
-:- INDUCTION: BY FUNGAL INFECTION.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon esculentum (Iomato). Bubryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                        Danhash N., Wagemakers C.A.M., van Kan J.A.L., de Wit P.J.G.M.;
"Molecular characterization of four chitinase cDNAs obtained from Cladosportum fulvum-infected tomato.";
Plant Mol. Biol. 22:1017-1029(1993).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
182 APCKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPK
                                                     Gl-JUN-1994 (Rel. 29, Created)
(J-UJN-1994 (Rel. 29, Last sequence update)
(1-CCT-1994 (Rel. 30, Last anotation update)
BASIC 30 KDA ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
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-!-CATALTYTIC ACTIVITY: HUTROLYESIS OF THE 1,4-BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
-!- EVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAFURS OR STEMS
SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE
SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 HDVIIGRWQPSGADQAANRVPGFGVITNIINGGLECGHGSDSRVQDRIGFYRRYCGILGV 299
                                                                                                                                                                                                                                                                                                                                                                                                                         --GPGPSGDLGGV---ISNSMFDQMLNHRNDNACQGKNNFYSYNAFVTAAGSFPGFGTTG 119
                                                                                                                                                                                                                                                                                                                                                                                                      125 STDVKKREVAAFLAQISHETIGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPG 184
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                       68 VPVPTPSG--GGVSSIISQSLFDQMLLHRNDAACLAK-GFYNYGAFVAAANSFSGFATTG 124
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                                                                                                                                                                                                                                                                        9 MLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGTP 67
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-i- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHIIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 KKYFGRGPIQISHNYNYGPAGQAIGTDLINNPDLVASDATVSFKTALWFWMTPQSPKPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV
                                                                                                                                                                                                                                                                                                     11 LLFSVLLLSASAEQCGSQAGGALCASGLCCSKFGWCGNTNEYCGPGNCQSQCPG----
                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                       70.7%; Score 1248.5; DB 1; Length 322; 72.6%; Pred. No. 6.9e-87; Live 25; Mismatches 46; Indels 15;
                         REMOVED IN MATURE FORM.
CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBL_TaxID=4113;
             BASIC 30 KDA ENDOCHITINASE.
                                                                                                                                           DROXYLATION (POTENTIAL). D13A9191AEE8FC5A CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
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STRAIN-CV. DATURA; TISSUE-Leaf;
MEDLINE-94154255; PubMed-8111037;
                                                                                                                                                           34345 MW;
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                                                                                                                                                                                                           Query Match
Best Local Similarity 72.64
Matches 228; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                             247 VITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD 246
-:- INDUCTION: IN RESPONSE TO INFECTION, ELLCITOR, ETHYLENE, WOUNDING.
-:- SIMILARITY: BELONGS TO CHITINAGE CLASS IN WHICH IS SIMILAR TO CLASS IB IN THE CAPALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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33629 MW;
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P21226;
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                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papillonoideae; Vicieae; Pisum.
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PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                      CONTAINING FUNGAL PATHOGENS.
-!- CATALTTIC ACTUITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
N-ACETYL-O-GLUCOSAMINE POLYMERS OF CHIIN.
-!- INDUCTION: BY FUNGAL INFECTION.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERNINAL
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERNINAL
CHITIN-BINDING LEGILN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
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                                                                                                                                                                                                                                                                                                                                    chitinase mRNA from pea leaves (Pisum sativum L.) inoculated with Associated pisi Lib.";
Plant Sci. 92:69-79(1993).
-i- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. BIRTE; TISSUE-Leaf;
Vad K., de Neergaard E., Madriz-Ordenana K., Mikkelsen J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
                                                                                                                                                                                                                                                                                            Collinge D.B.; "Accumulation of defence-related transcripts and cloning of
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ENDOCHITINAGE.
CHITIN-BINDING (BY S.
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               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE PRECURSOR (EC 3.2.1.14)
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InterPro; IPR001026; Glyco_hydro_19.
Pfam, PP00187; Chitin_binding; 1.
Pfam, PP00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000654; Glyco_hydro_19; 1.
Probom; PD000669; Chitin_bind; 1.
SMART; SM00270; ChtBD1; 1.
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                                                                                                   Pisum sativum (Garden pea)
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                                                                                                                                                                   SGADQAAGRVPGYGVIINIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSYGDNLDCYN 314
                                                                                                                                                                                                                                                                                                                                      SAADSSAGRVPGYGVITNIINGGIECGHGQDNRVDDRVGFYKRYCQIFGVDPGGNLDCNN 315
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MEDLINE=95306779; PubMed=7787175;
Chang M.M., Borovitz D., Culley D., Hadwiger L.A.;
Chang M.M., Horovitz D., Culley D., Hadwiger L.A.;
"Molecular cloning and characterization of a pea chitinase gene expressed in response to wounding, fungal infection and the elicitor
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SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO SIMILARITY: BELONGS TO PART BUT WHICH INCLUDE A N-TERMINAL CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
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STRAIN-CV. BIRTE; TISSUE-Leaf;
Vad K., Mikkelsen J.D., Collinge D.B.;
"Induction, purification and characterization of chitinase isolate from pea leaves incoulated with Ascochyta pisi.";
Planta 184:24-29(1991).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
-:- TOWNINING FUNGAL PATHOGENS.
--- TOWNINING FUNGAL PATHOGENS.
                                                                                                                       195 ISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHDVITGRWSP
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15-JUL-1999 (Rel. 38, Last annotation update)
ENDOCHITINASE A2 PRECURSOR (EC 3.2.1.14).
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InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
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Plant Mol. Biol. 28:105-111(1995).
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CHILIN-BINDING (BY SIMILARITY).
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                                                                                                                                                                                                                                                     TPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGS 125
                                                                                                                                                                                                                                                               TDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGK 185
                                                                                                                                                                                                                                                                                                          TATKKREIAAFLGQTSHETTGGWPTAPDGPYAWGYCFLREQN-PSTYCQASSEFPCASGK 174
                                                                                                                                                                                                                                                                                                                           KYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSH 245
                                                                                                                                                                                                                                                                                                                                        DVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVS 305
                                                                                                                                                                                                                                                                                                                                                                           "Sequence analysis of a genomic clone encoding an endochitinase from Solanum tuberosum.";
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                7 VAMLAAAFAVS-AHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGCSGG 65
                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                            Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                        PROSITE; PS00026; CHITIN, BINDING; 1.
PROSITE; PS00773; CHITINASE 19_1; 1.
PROSITE; PS00774; CHITINASE 19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Multigene family; Signal.
                                                                                                                                                                                               54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Asteridae; eusaterids I; Solanales; Solanaceae; Solanum
NCBL_TaxID=4113;
                                                                                                                                                                            DB 1;
                                                                                                                                                                           68.4%; Score 1208; DB 1
69.0%; Pred. No. 7.6e-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 09, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 AA
                                                                                                                                                                                     Pred. No. 7.66
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 17:5855-5855(1989)
        4; Glyco_hydro_19; 1.
ChtBD1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. RUSSET BURBANK;
MEDLINE-89345190; PubMed-2762165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CV. RUSSET BURBANK;
MEDLINE-88262525; Pubmed=3387233;
                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09, Created)
                                                                                                                                      59 E
PRINTS; PR00451; CHITINBINDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaynor J.J., Unkenholz K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Solanum tuberosum (Potato).
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                          309
324
62
62
44
51
                                                                                                                                                                                                                                                                                                                                                                                                                 306 YGDNLDCYNQRPF 318
                                                                                                                                                  AA;
                                                                                                                                                                                     Similarity
          PD000574;
                  SM00270:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1988
01-OCT-1996
                                                                                                                                                                                             Matches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHIT_SOLTU
                                                                                 CHAIN
PROPEP
DOMAIN
DISULFID
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Best Local (
                                                                                                                               DISULFID
                                                                                                                      DISULFID
                                                                                                                                        DISULFID
                                                                                                                                                SEQUENCE
                                                                        SIGNAL
                   SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
CHIT_SOLTU
                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                        126
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"Primary structure of an endochitinase mRNA from Solanum tuberosum.";
Nucleic Acids Res. 16:5210-5210(1988).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 SGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 TGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 VAYLLFSLLVLVSAALAQNCGSQGGGKACASGQCCSKFGWCGNTNDYCGSGNCQSQ---C 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 VAMLAAAFAV---SAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGC 62
                                                                                                    -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYLD-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
-!- INDUCTION: BY ETHYLENE.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO PAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REMOVED IN MATURE FORM (PROBABLE). CHITIN-BINDING (BY SIMILARITY). BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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669B82159BC176EF CRC64;
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HSSP; P23951; 2BAA.
HSPP: P23951; 2BAA.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR00105; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
PRINTS; PR00142; Glyco_hydro_19; 1.
PRINTS; PR00421; CHITINBLONG.
ProDom; PD000654; Glyco_hydro_19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00270; ChtBbl; 1.
PROSITE; PS00026; CHTINL BINDING; 1.
PROSITE; PS00773; CHTINASE_19_1; 1.
PROSITE; PS00774; CHTINASE_19_2; 1.
                                                                                   CONTAINING FUNGAL PATHOGENS.
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35406 N
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218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 AA;
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SIGNAL
                                                                                                                                                                                                                                                                                                 HYDROLASES).
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DISULFID
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Query Match
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CHI4_SOLTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P27275; IMMC.
Interpro; PR00102; Chitin_bind.
Interpro; PR00102; Chitin_bind.
Interpro; PR00102; Chitin_bind.
Pfam; PR00187; Chitin_binding, 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR000574; Glyco_hydro_19; 1.
PRODOM; PD000609; Chitin_bind; 1.
PROSTER; S800026; CHITIN_BINDING; 1.
PROSTER; PS00026; CHITIN_BINDING; 1.
PROSTE; PS00774; CHITINASE_19_1; 1.
PROSTE; PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV HAVANA 425; TISSUE=Leaf; BARDINE=29269767; PubMed=1588915; VanbLinne=29269767; PubMed=1588915; Van Buuren M., Neuhaus 7.-M., Shinshi H., Ryals J., Meins F. Jr.; Van Buuren M., Neuhaus J.-M., Shinshi H., Ryals J., Meins F. Jr.; The structure and regulation of homeologous tobacco endochitinase genes of Nicotiana sylvestris and N. tomentosiformis origin."; Mol. Gen. Genet. 233.460-469(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS (PROBABLE).
SIMILARATIY: BELONGS TO CHTINARE CLASS IA WHICH IS SIMILAR TO
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                        Embryophyta; Tracheophyta;
dons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REMOVED IN MATURE FORM (PROBABLE). CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTAINING FUNGAL PATHOGENS.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
W; 4F684CEIFBD432FB CR644;
                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-CCT-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE 3 PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENDOCHITINASE 3.
                                                                                                                                                   334 AA
                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                   Nicotiana tabacum (Common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multigene family.
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                      GVSYGDNLDCYNQRPF 318
                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327
334
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41
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                                                                                                                                              CHI3_TOBAC
P29059;
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SEQUENCE
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SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
DEVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OLD ROOT SEGMENTS, AND CARPELS.
INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLIDE A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                     123
                                                               Gaps
                                                                                                                                                                                     70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. DATURA; TISSUE-Leaf;
MEDLINE=94154255; PubMed=3111037;
MEDLINE=94.54255; PubMed=3111037;
MERCALL & COMPLINK E.; ACMPLINK MOLE BIOL. 24:353-367(1994).
-1. FUNCTION: THIS PROTEIN FUNCAL.
CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                 SILVILFILLAVSAEQCGKQAGGARCPSGMCCSNFGWCGNTQDYCGPGKCQSQCPSGFGPT
                                                                                                                                                                                                                                                                                              251 CHDVITGRWIPSAADRAANRLPGYGVITNIINGGLECGHGSDARVQDRIGFYRRYCSILG
                                                                                                                                                                                                                                                         ---PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATT
                                                                                                                                                                                                                                                                                                                                                                                     GSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 SHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGODGRVADRIGFYKRYCDLLG
                                                                                                                            8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
                                                                   4,
   Length 334;
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 4 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
68.3%; Score 1206; DB 1; 67.9%; Pred. No. 1.1e-83; ive 32; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 AA
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01-0CT-1996 (Rel. 34, Last sequ
01-0CT-1996 (Rel. 34, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Solanum tuberosum (Potato)
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 VSYGDNLDCYNORPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 VSPGDNIDCGNOKSF 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4113;
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                                        Best Local Sin
Matches 214;
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214;
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Best Local S
Matches 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DISULFID
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q_{\overline{Y}}
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 agreement (See http://www.isb-sib.ch/announce/
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Bukaryota, Viidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 GTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAK-GFYNYGAFVAAANSFSGFATT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 KPPTPGPGPSGGDIGSVISNSMFDQMLKHRNDNACQGKNNFYSYNAFINAARSFGGFGTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 SHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHDVIICRWQPSAADRAANRLPGFGVITNIINGGLECGRGSDSRVQDRIGFYRRYCGI 302
                                                                                                                                                                                                          SMART; SM00270; ChtBbl; I.
PROSITE; PS00026; CHTIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin_degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 VAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQC-NGCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=94143492; PubMed=8310072;
Hamel F., Bellemare G.;
"Nuclectide sequence of a Brassica napus endochitinase gene.";
Plant Physiol. 101:1403-1403(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         έ'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 302;
                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                              54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
01-0cT-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE CH25 PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 AA
entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                             Interpro; IPR000726; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
Probom; PD000574; Glyco_hydro_19; 1.
Probom; PD000609; Chitin_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                            InterPro; IPR001002; Chitin_bind.
                                                          EMBL; U02608; AAA17410.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 210; Conserv
                                                                            HSSP; P23951; 2BAA.
                                                                                                                                                                                                                                                                                    Hydrolase; Glycosi
Multigene family.
NON_TER 1
SIGNAL <1
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Q09023;
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DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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BRANA
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Matches
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BRIDGHIS BRID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 NGCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 FATIGSIDVKKREVAAFLAQISHETIGGWPTAPDGPYSWGYCFNQERGAISDYCTPSSQW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GGTP-PGPT----GDLSGIISRSQFDDMLKHRNDNACPARGFYTYDAFINAAKSFPG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BININING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRGVVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYC-GTGCQSQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.6%; Score 1192.5; DB 1; Length 322; 66.9%; Pred. No. 1.1e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E62EE4B17211DBCD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.1e-82;
; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENDOCHITINASE C
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001002; Chitin_bind.
InterPro; IPR001026; Glyco_hydro_19.
Pfam, PF001087; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; I.
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
SMART; SM00270; ChtBD1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00026; CHITIN_BINDING; PROSITE; PS00773; CHITINASE_19_1; PROSITE; PS00774; CHITINASE_19_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39:
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62 (
38 E
44 E
51 B
60 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLLGVSYGDNLDCYNQRPFA 319
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                                                                                                                                                                                                                                                                                                                                                                          EMBL; M95835; AAA32986.1; -.
HSSP; P23951; 2BAA.
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ne: 917 sec
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GenCore version 4.5
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using sw model - protein search, OM protein 3, 2002, 18:47:01; Search time 157:87 Seconds (without alignments) 295.565 Million cell updates/sec May Run on:

US-09-534-229C-3 1765 1 MRGVVVVAMIAAAFAVSAHA......DLLGVSYGDNLDCXNQRPFA 319 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

473505 Total number of hits satisfying chosen parameters: 473505 seqs, 146272329 residues Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

SPTREMBL_17:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:* sp_organelle:*
sp_phage:*
sp_plant:* sp_rodent:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:* sp_virus:*
sp_vertebrate:*

SUMMARIES

		ď			SUMMAKIES	
Result No.	Score	Query Match	ğ Query Match Length DB	DB	ΔΙ	Description
	1696.5	1.96	320	10	041539	Q41539 triticum ae
5	1675.5	94.9	318	10	Q9AXR9	Q9axr9 secale cere
er,	1597	90.5	320	10	69S6O	Q9sq13 poa pratens
4	1557	88.2	340	10	Q9SQL4	
S	1421	80.5	321	10	Q9FRV1	
Q	1359.5	77.0	323	10	042993	Q42993 oryza sativ
7	1352.5	76.6	320	10	042994	-
80	1317.5	74.6	340	10	Q43294	-
O	1305	73.9	326	10	P93680	P93680 persea amer
10	1291.5	73.2		10	042839	Q42839 hordeum vul
11	1279	72.5	333	10	042992	Q42992 oryza sativ
12	1274	72.2		10	042995	Q42995 oryza sativ
13	1272.5	72.1		10	040667	Q40667 oryza sativ
14	1260	71.4		10	041180	
15	1256	71.2	32	10	Q9FS45	Q9fs45 vitis vinif
16	1253	71.0		10	Q9FEW1	_
17	1239.5	70.2	31	10	038777	Q38777 allium sati
18	1237	70.1	320	10	Q9SDY6	Q9sdy6 glycine max
19	1236	70.0	33	10	Q42970	

Q9m7f5 arabis pari	7				Q38776 allium sati	-							Q9sxj4 arabidopsis			arabidop		Q9sxj3 arabidopsis	arabis	_	cacar		vigna	aı	081144 solanum tub
09M7F5	P93327	P94084	Q9FXL8	Q9M7H2	038776	042428	081145	Q9M7H0	098735	095838	O9M7H4	043179	Q9SXJ4	Q9M7G4	Q9M7G9	Q9SXJ2	Q9M7G7	Q9SXJ3	Q9M7G2	Q9M7F4	080404	Q92TK4	Q9FUH3	Q9ZP10	081144
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
312	325	327	315	305	302	316	329	326	335	335	308	315	335	302	310	335	320	335	306	312	311	325	297	328	329
68.5	68.5	68.4	68.3	68.3	68.2	68.0	67.9	67.7	67.5	67.5	67.4	67.2	67.2	67.2	67.2	67.2	67.1	67.1	67.1	66.9	6.99	66.7	66.5	66.4	66.1
1208.5	1208.5	1207.5	1206	1205.5	1203.5	1200.5	1198.5	1194.5	1190.5	1190.5	1189.5	1186.5	1186.5	1185.5	1185.5	1185.5	1185	1184.5	11.83.5	1181.5	1180	1177	1174.5	ä	1167.5
20	21	22	23	24	25	26	27	28	29	30	31	32	8	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENDOCHTINASE PRECURSOR.
Triticum aestivum (Wheat).
                                                                                                                                                                                                                                                                                     ESOURNCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIL-CY. CHINESE SPRING;
Liao Y.C., Kreuzaler F., Fischer R., Reisener H.J., Tiburzy R.;
Plant Sci. 103:177-187(1994).

REMBL; X76041; CAA53626.1;
REMBL; X76041; CAA53626.1;
REMBL; X76041; CAA53626.1;
REMBL; X76041; CAA53626.1;
REMBL; ROOUSC; CHILID.bind.

RICHEPRO; PRO00072; CHILID.bind.

PERM; PRO0182; Glyco.hydro.19.
PFam; PRO0182; Glyco.hydro.19; 1.
PRODOM; PRO00651; CHITINENING.

PRODOM; PRO006574; Glyco.hydro.19; 1.
PRODOM; PRO0060974; CHITIN.BINDING; 1.

PROSITE: FS00074; CHITIN.BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 ENDOCHITINASE.
33602 MW; F258D9DD8EF65E0E CRC64;
                                       320 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                       PRT;
                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chitin-binding; Signal.
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                                  Q41539
Q41539;
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RESULT
                       041539
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Ϊ; Gaps Query Match
Best Local Similarity 95.3%; Pred. No. 1.5e-141;
Matches 305; Conservative 9; Mismatches 5; Indels 1;

us-09-534-229c-3.rspt

g Ω Qy

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KPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCD 300
          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.5%; Score 1597; DB 10; 90.3%; Pred. No. 8.8e-133; iive 15; Mismatches 14;
                                                                                                                                        Ä.
                                                                                                                                        320
                                                                                                                                                                                                                                                                                                                                                                                                             Pfan; PP00187; chitin_binding; 1.
Pran; PP00182; Glyco_hydro_19; 1.
PRINTS; PR00421; GHYDINBINNG.
ProDom; PD0006574; Glyco_hydro_19; 1.
SYART; SM00270; ChtBni, bind; 1.
PROSITE; PS00773; CHTRINASE_19_1; 1.
PROSITE; PS00774; CHTRINASE_19_2; 1.
PROSITE; PS00774; CHTRINASE_19_2; 1.
PROSITE; PS00026; CHTRINASE_19_2; 1.
Chitin-binding;
                                                                                                                                                                                                                                                                                                                                   Du M., Ha S.B.;
Submitted (APR-1997) to the EMBL/Gen
EMBL; AF000966; ARF04454.1; -.
HSSP; P23951; 2BAA.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
                                                                                                                                                                                                                                Poa pratensis (Kentucky bluegrass).
                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLLGVSYGDNLDCYNQRPF 318
                                                               LLGVSYGHNLDCYNQRPFA 318
                                                  LLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 90.33
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=GLADE;
                                                                                                                                                                                                                                                                                 NCBI_TaxID=4545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                          Q9SQL3
Q9SQL3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGF 120
                                                   119
                                                                                                                            180
                                                                                                                                                     239
                                                                                                                                                                                                       PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, NCBL_TaxID-4550,
                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=20532799; PubMed=11060301;
MEDLINE=20532799; PubMed=11060301;
MEDLINE=20532799; PubMed=11060301;
Sarhan F., Moffatt B., Griffith M., Xiong F., Yang D.S.C., Wiseman S.l. Sarhan F., Danyluk J., Xue Y.Q., Hew C.L., Doherty-Kirby A., Lajoie G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRGVVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTGGTDVRKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAPSDYCSPSSQWP
                FATTGGADVRKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAASDYCSPNSQW
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                                                   GCS-GGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSG
                                                                                                     FATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQW
                                                                                                                                                       PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS
  MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Chitinase genes responsive to cold encode antifreeze proteins
                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
31.7 KDA CLASS I ENDOCHITINASE-ANTIFREEZE PROTEIN PRECURSOR.
Secale cereale (Rye).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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BA685E1DB7A58E63 CRC64;
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                                                                                                                                                                                                                                                                                                                                                    Ā
                                                                                                                                                                                                                                                                                                                                                  318
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EMBL; AF280437; AAG53609.1; -.
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33636 MW;
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                                                                                                                                                                                                                                                                        DELGVIYGDNEDCYNQRPFA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 AA;
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SIGNAL
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PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 299
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 320;
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                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                     320 AA; 33711 MW; BEFC3ADBFEC939B5 CRC64;
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298 YCDLLGVSYGDNLDCYNQRPFA 319
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                                                                                                                                                                                                                                     321 AA; 33641 MW;
                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 78.9%
Matches 254; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
STRAIN=NIPPONBARE;
                                                  Triticeae; Secale.
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4530;
SEED CHITINASE-A.
                                                           NCBI_TaxID=4550;
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                                                                                                                                                                                                                                    SEQUENCE
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Q42993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GCSGGTPVPVPTPS-GGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 FATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGR--VADRIGFYKR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRGLVVVAILVAAPARAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGNTSDYCGTGCQSQCN 60
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                             Eukaryota, Viridiplantãe, Střeptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
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                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                    Du M., Ha S.B.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF000964; AAF04453.1; -.
HSSP; P23951; 2BAA.
                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                        Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                88.2%; Score 1557; DB 10;
larity 87.9%; Pred. No. 3.1e-129;
Conservative 17; Mismatches 18;
                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 AA
                               340 AA
                                                                                                                                                                                                                          Interpro; IPR001002; Chitin_bind.
Interpro; IPR001026; Glyco_hydro_19.
Pfam; PP00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PKINTS; PR00451; CHTRINBINDNG.
PRODOM; PD0000574; Glyco_hydro_19; 1.
ProDom; P0000674; Glyco_hydro_19; 1.
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                                                    Created)
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                                                                                                      Poa pratensis (Kentucky bluegrass).
                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 YCDLLGVSYGDNLDCYNESPF 320
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                                                  01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                 SMART; SM00270; ChtBD1;
                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=4545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                                            STRAIN-GLADE
                                                                                                                                                                                                                                                                                                                                                                                                     282;
                                                                                                                                    Poa.
                                                                                  CHITINASE.
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Best Local 9
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                                           09SQL4;
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                               Q9SQL4
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            4
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ID 099
AC 099
DT 011
DT 011
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118 SGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GC-SGGTPV-PVPTPS-GGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
Secale cereale (Rye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta:
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QWPCAPGXKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 321;
                                                                                                                                                                                              Ohnuma T. Yanagami T., Ishiguro M.;
Ohnuma T., Yanagami T., Ishiguro M.;
"Cloning and Sequencing of the Rye Seed Chitinase.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB051578, BAB18519.1;
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
IPRMS; PR00481; CHITINBINDWG.
ProDom; PD000674; Glyco_hydro_19; I.
PRINTS; PR00451; CHITINBINDWG.
ProDom; PD000609; Chitin_bind; I.
SWART; SW00270; Chitin_bind; I.
SWART; SW00270; Chitin_bind; I.
Chitin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (Tremblrel. 01, Created)
01-NOV-1996 (Tremblrel. 01, Last sequence update)
01-NOV-1996 (Tremblrel. 17, Last sequence update)
ENDOCHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (POLY-N-ACETYLELUCOSAMINIDASE) (POLY-HETA-GLUCOSAMINIDASE)
CHIAI OR CHT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.5%; Score 1421; DB 10; Length 78.9%; Pred. No. 2.8e-117; cive 29; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76E5902BBC337C8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE-94049667; PubMed-7901749;
Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
"Sequence variation, differential expression and chromosomal location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 GGCGGGTPPSSGGGSGVASIISPSLFDQMLLHRNDQACAAKGFYTYDAEVAAANAYPDF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1,4-BETA-POLY-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQE-RGATSDYCTPSSQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCSGGTPVPVPTPSGGGVSSIISOSLFDOMLLHRNDAACLAKGFYNYGAFVAAANSFSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 320;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENDOCHITINASE.
D7331BF4A6B592E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLEEL. 01, Created)
01-NOV-1996 (TrEMBLEEL. 01, Last sequence update)
01-NOV-1996 (TrEMBLEEL. 17, Last annotation update)
CHTITARE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE)
ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1352.5; DB 10;
Pred. No. 3e-111;
...--+ches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chitin-binding; Glycosidase; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Mismatches
                                                                                                                                                                                 MOI Gen. Genet. 241:1-10(1993).

EMBL; D16223; BAA03751.1; -.

EMBL; D16223; BAA03751.1; -.

EMBL; D16223; BAA03751.1; -.

Mendel: 1582: Orysa.Chial.1582.

InterPro; PR000102; Chitin_bind.

Pfam; PF00187; chitin_binding; 1.

Pfam; PF00187; chitin_binding; 1.

PFINTS; PR00451; CHTTINBIRDNG.

PRODOM; PD0006574; G1yco_hydro_19; 1.

PRODOM; PD000699; Chitin_bind; 1.

PROSITE; PS00773; CHTINASE.19_1; 1.

PROSITE; PS00774; CHTINASE.19_2; 1.

PROSITE; PS00774; CHTINASE.19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
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                                                                                                                                                                         rice chitinase genes.";
1. Gen. Genet. 241:1-10(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33681 MW;
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75.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 DMLGVSYGDNLDCYNQRPY 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                             STRAIN-NIPPONBARE;
                                   NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHIA1 OR CHI-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q43294
Q43294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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   MEDLINE=94049667; PubMed=7901749;
Nishikawa Y., Kishimoto N., Saito A., Hibi T.;
"Sequence variation, differential expression and chromosomal location
of rice chitinase genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G-CSGGTPVPVPTPSGG---GVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 FSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAT--SDYCT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 FPSFATTGDAATRKREVAAFLAQTSHETTGGWATAPDGPYSWGYCFKEENNGNVGSDYCV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 PSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFW 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UDN-2001 (TrEMBLrel. 17, Last annotation update)
01-UDN-2001 (TREMBLRE). 17, Last annotation update)
ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
CHIAL OR CHIA-3.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                           CSTRAIN—CV. NIPPONBARE;

AN ISHIZAWA Y., HIDI T.;

ALTALITICATIVITY: HURBOLYSIS OF THE 1,4-BETA-LINKAGES OF N-1-CATALITIC ACTIVITY: HURBOLYSIS OF CHITIN.

ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

BENEL; D16221, BAA303749-11;

BENEL; X56063; CAA39535-11;

RSSP; P23951; 2BAA.

Mandel; 14776; Orysa; Chial; 14776.

InterPro; IPRO01002; Chial; Dind.

InterPro; IPRO01002; Chial; Dind.

Pfam; PF00182; Glyco_hydro_19;

Pfam; PF00182; Glyco_hydro_19;

Pfam; PR00182; Glyco_hydro_19;

PRINTS; PR00451; CHITININNAC.

PRODOM; P00006574; Glyco_hydro_19;

PRODOM; P00006574; CHITININNAC.

PROSITE; PS000773; CHITININASE_19_1; 1.

PROSITE; PS000773; CHITININASE_19_2; 1.

PROSITE; PS000774; CHITININASE_19_2; 1.

PROSITE; PS00076; CHITININASE_19_2; 1.

PROSITE; PS000776; CHITININASE_19_2; 1.

PROSITE; PS00076; CHITININASE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 QSSQWPCAAGKKYYGRGPIQISYNYNYGPAGQAIGSNLLSNPDLVASDATVSFKTAFWFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRALAVVVVATAFAVVAVVGEQCGSQAGGALCPNCLCCSQYGWCGSTSAYCGSGCQSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.0%; Score 1359.5; DB 10; Lengt 75.6%; Pred. No. 7.3e-112; ive 27; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1C85B6227A33EB06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENDOCHITINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 YKRYCDLLGVSYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 YKRYCDMLGVSYGANLDCYNQRPF 321
                                                                           Gen. Genet. 241:1-10(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33764 MW;
                                                                                                                 SEQUENCE OF 21-323 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 77.0%
Best Local Similarity 75.6%
Matches 245; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Q42994
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9 Gaps

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Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Persea
                                                                                                                                                                                                                                                                         26 326 E
326 AA; 34586 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYGSNLDCYNQRSF 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYGDNLDCYNQRPF 318
                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticeae; Horder
NCBI_TaxID=4513;
[1]
           NCBI_TaxID=3435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHIA1 OR CHI33.
                                                                                                                                                                                                                                                                                                                                 Best Local Sim
Matches 230;
                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                     Query Match
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Q42839;
                                                                                                                                                                                                                                                                SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishizawa Y., Kishimcto N., Saito A., Hibi T.;
Nishizawa Y., Kishimcoto N., Saito A., Hibi T.;
"Sequence variation, differential expression and chromosomal location of rice chitinase genes.";
Mol. Gen. Genet. 241:1-10(1933).
-!- CAPALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
EMBL. X56787; CAA40107.1;
--- EMBL: D16222; BA037501.1;
--- HSSP; P23951: 2BAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFAIT 123
                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           4 VVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGCS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                       16 IVALAVIAAALATAARAEQCGAQAGGARCPNCLCCSRWGWCGTTSDFCGDGCQSQCSGC-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 GSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPS
                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                        50; Indels
                                                                                                                                                                                                                                                                                                                                      CHITINASE.
642F13E3928CA7BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
3.2.1.14).
                                                                                                                                                                      Mendel, 727; Orysa; Chial; 727.
InterPro; IPR00102; Chitin_bind.
InterPro; IPR00102; Chitin_bind.
InterPro; IPR00102; Chitin_bind.
InterPro; IPR00102; Chitin_binding; I.
Pfam; PF00187; Chitin_binding; I.
Propom; PF00189; Chitin_bind; I.
ProDom; PF001059; Chitin_bind; I.
SMART; SM00451; CHITINASE_19, I.
PROSITE; PS00774; CHITINASE_19_2; I.
PROSITE; PS00774; CHITINASE_19_2; I.
PROSITE; PS00026; CHITINASE_19_2; I.
PROSITE; PS00026; CHITINASE_19_2; I.
Chitin_binding; Glycosidase; Hydrolase; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                74.6%; Score 1317.5; DB 10
72.4%; Pred. No. 3.8e-108;
iive 36; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                  STRAIN=JAPONICA, CV. NIPPONBARE;
MEDLINE=94049667; Pubmed=7901749;
                                                                                                                                                                                                                                                                                                                                                340 AA; 35586 MW;
       Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, 01-AUG-1998 (TrEMBLrel. 07, 01-JUN-2001 (TrEMBLrel. 17, ENDOCHITINASE PRECURSOR (EC CHIAI OR CHII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Persea americana (Avocado)
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.6%
Best Local Similarity 72.4%
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 VSYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 IGTGGNLDCYNQRPF 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      340
                                        SEQUENCE FROM N.A.
        Ehrhartoideae; 0
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                      CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P93680
P93680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
P93680
ID P93680
DT 001
DT 01
DD EN
DD CH
        δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
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SEQUENCE FROM N. A.

SEQUENCE FROM N. A.

SEQUENCE FROM N. A.

SOWAS S., Hsieh L., Krebitz M., Akasawa A., Martin B., Starrett D.,

SOWAS S., Hsieh L., Krebitz M., Akasawa A., Martin B., Starrett D.,

SOWAS S., Hsieh L., Krebitz M., Akasawa A., Martin B., Starrett D.,

Sowas S., Hsieh L., Krebitz M., Akasawa A., Martin B., Starrett D.,

Receptor C., Scheiner O., Breiteneder H.;

BMBL; 278202; CAB01591.1; --

RMSP; P02877; HHV.

Medel; 14766; Perae, Chial; 14766.

InterPro; IPR001002; Chitin_bind.

RICHERO: IPR001002; Chitin_bind.

Refam; PF00187; Chitin_binding; 1.

ProDom; P00187; Chitin_bind; 1.

RYMRT; SM00270; Chitin_bind; 1.

SMART; SM00270; Chitin_bind; 1.

SMART; SM00270; CHITINASE_19_1; 1.

RROSITE; PS00774; CHITINASE_19_2; 1.

RROSITE; PS00774; CHITINASE_19_2; 1.

Chitin-binding; Clycostdase; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 SIDVKKREVAAFLAQISHETIGGWPIAPDGPYSWGYCFNQERGAISDYCIPSSQWPCAPG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LILLLLVGLLAGEAFAEQCGRQAGGALCPGGLCCSQFGWCGSTSDYCGFTCQSQCGGV-- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 VVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGCSG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-UJUN-2001 (TIEMBLIEL. 17, Last annotation update)
CHITIMASE (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENDOCHITINASE.
643B20589E062E61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. Similarity 73.2%; Score 1305; DB 10; Similarity 73.2%; Pred. No. 4.6e-107; 30; Conservative 35; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Plant J.

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180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGGGGGGGGGGGAVEAVSKELFEQLLLHRNDAACPARGFYTYDAFVTAAAAFPDF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1,4-BETA-POLY-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 CAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 VAMLAAAFAVSAH--AEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTPVPVPTPSGGG-----VSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGF
                                                                                             ż
                                                                                             G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 333;
SEQUENCE FROM N.A.
STRAIN=IR36, TISSUE=ETIOLATED LEAF;
YUN C.H., Kim J.K., Park Y.H.;
Submitted (NOV-1294) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES GENEL, L37289; AASI377.1,
HSSP; P23951; ZBAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E2B65D4155B8C73D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.5%; Score 1279; DB 10; 71.7%; Pred. No. 9.2e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chitin-binding; Glycosidase; Hydrolase; SIGNAL 1 23
                                                                                                                                                                                Medel; 26; Orysa; Chial; 26.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001025; Glyco_hydro_19.
Pfam; PP00187; Chitin_binding; I.
Pfam; PP00182; Glyco_hydro_19; I.
ProDom; PD000574; CHITINBINNG.
ProDom; PD000609; Chitin_bind; I.
PROSITE; PS00773; CHITINASE_19_1; I.
PROSITE; PS00774; CHITINASE_19_1; I.
PROSITE; PS00774; CHITINASE_19_2; I.
PROSITE; PS00026; CHITIN_BINDING; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHITINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34336 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 VLGIGYGSNLDCYDQRPF 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 LLGVSYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=IR36; TISSUE=LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHIA1 OR RC24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sim:
Matches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         042995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 042995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LWFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGTGVITNIINGGLECGRGQDGRVAD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHTILNASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCQSQCNGCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRN---DAACLAKGFYNYGAF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAAANSFSGFATIGSIDVKKREVAAFLAQTSHETIGGWPTAPDGPYSWGYCFNQERGATS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRGPSVVVAIVAIVAIVLSAALAMAMVVRAQQGGSQAGGATCPNCLCCSRFGYCGSTSDYCGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TAXID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRG-----VVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAAAATFPAFGTTGSTETRKQEVAAFFGQTSHETTGGWATAPDGPYSWGYCYRRELGSPP
                                                                                                                                                                                TABLE 1. S13/3-293(1374).

TABLE 1. S13/3-293(1374).

RESTAL-D-GLUCCSAMINE POLYMERS OF CHITIN.

EMBL: J134211, AAA56787.1;

RASSP: P23951, 2BAA.

RAGETYL-D-GLUCCSAMINE POLYMERS OF CHITIN.

RASSP: P23951, 2BAA.

RAGETISE: RAGETISE 2BAA.

RAGETISE: RAGETISE 2BAA.

RAGETISE 2BAA.

RAGETISE 2BAA.

RAGETISE 2BAA.

RAGETISE 2BAA.

RAGETISE PROUBLY: LALL DIAG.

REPORT PROUBLY: CHITINBINDNG.

PRODOW: PROUBLY: CHITINBINDNG.

PRODOW: PROUBCY: CHITINBINDNG.

RART: SMO0270; CHEDI: 1.

RAGETISE PSOU74; CHITINASE 19-1; UNKNOWN.

REPORTE: PSOU74; CHITINASE 19-2; 1.

RAGETISE PSOU74; CHITINASE 19-2; 1.

RAGITE: PSOU74; CHITINASE 19-2; 1.

RAGITE: PSOU774; CHITINASE 19-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.2%; Score 1291.5; DB 10; Length 332; 71.6%; Pred. No. 7.3e-106; Live 33; Mismatches 43; Indels 17;
                                                                                                                                                                                            OF
                                                                                                                       "Identification of an enhancer/silencer sequence directing the aleurone-specific expression of a barley chitinase gene.";
                                                                           J., Raikhel N.V.,
                                                                         Leah R., Skriver K., Knudsen S., Ruud-Hansen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIGFYKRYCDLLGVSYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                     MEDLINE=95078949; PubMed=7987416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                   6:579-589(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 235; Conserv
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Query Match

Matches

54 61

g δ q QY 114

P

231 234 291

a δ

 δ

g

042992 042992

RESULT 11

g

5;

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RYCDLLGVSYGDNLDCYNORPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 RYCDMLGVSYGANLDCYNQRPF 317
                                                                                                                                                                                                                                                                                                                                                                               Query Match 72.1
Best Local Similarity 73.0
Matches 235; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
  ISSP; P23951; 2BAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASIC CHITINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996
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  4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RQLRRRRPDRPSGG------GGSGVASIVSRSLFDQMLLHRNDAACPAKNLYTYDAFV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDYCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NGCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
MEDLINE-96189256; PubMed-8605293;
Xu Y., Zhu Q., Panbangred W., Shirasu K., Lamb C.;
"Regulation, expression and function of a new basic chitinase gene
                                                               Trice (Oryza satiraz) 1...;

E plant Mol. Biol. 30:387-401(1996).

- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLOCOSAMINE POLYMERS OF CHITIN.

E MEDI; X87109; CAA60590.1; -..

R HSSP; P23951; 2BA.

R HGAPPO; IPR001002; Chitin_bind.

R InterPro; IPR00102; Chitin_bind.

R InterPro; IPR00102; Chitin_bind.

R Pfam; PF00187; chitin_binding; 1.

R Pfam; PF00187; CHITINBIRNG.

R PFAMS; PR00451; CHITINBIRNG.

R PFODOM; PD000574; Glyco_hydro_19; 1.

R PRINES; PR00451; CHITINBIRNG.

R PRODOM; PD000674; Glyco_hydro_19; 1.

R PRODOM; PD0006774; Glyco_hydro_19; 1.

R PRODOM; PD0006774; Glyco_hydro_19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 AAANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 322 AA; 34505 MW; AD56FE9CF7D99B09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.2%; Score 1274; DB 10; 70.8%; Pred. No. 2.4e-104; tive 28; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chitin-binding; Glycosidase; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim Y., Baek J., Park H., Choi Y., kim S.;
Biosci. Biotechnol. Biochem. 0:0-0(1994).
EMBL; Z29961; CAA82849.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 DRIGEYKRYCDMLGVSYGANLDCYNQRPF 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 DRIGEYKRYCDLLGVSYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NoV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-UNN-2001 (TrEMBLrel. 17, Last and
CHITINASE CLASS I.
                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00774; CHITINASE_19_2; 1. PROSITE; PS00026; CHITIN_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 70.89
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4530;
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040667
AC 040667
AC 040667
DT 01-NOV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLINNPDLVASDATVSFKTALWFWMT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GSCGGGDPA---SGGASGVASIVSRSLFDQMLHRNDAACPAKNFYIYDAFVAAANAYP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.1%; Score 1272.5; DB 10; Length 319; 73.0%; Pred. No. 3.3e-104; Live 29; Mismatches 49; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chitin-binding.
SEQUENCE 319 AA; 33600 MW; C990572C114FC0A9 CRC64;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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Mendel; 1578; Orysa; Chial; 1578.
InterPro; IPR001002; Chitin bind.
InterPro; IPR001002; Chitin bind.
InterPro; IPR001025; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; I.
Pfam; PF00182; Glyco_hydro_19; I.
PRINKS; PR00451; CHITINBINDRG.
ProDom; PD000654; Glyco_hydro_19; I.
ProDom; PD000659; Chitin_bind; I.
PROSITE; PS00779; CHITINASE_19_1; PROSITE; PS00774; CHITINASE_19_2; I.
PROSITE; PS00774; CHITINASE_19_2; I.
PROSITE; PS0076; CHITINASE_19_2; I.
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Search completed: May
Job time: 886 sec
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
Vitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                            246
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                                                                                                                                                                                                                                                                                                                                                                                 127 DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK 186
                                                                                                                                                                                                                                                                                                                                                                                                 247 VITGRWSPSGADQAAGRVPGXGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
                                                                                                                                                                                                                                                                                                                      67 PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular characterization of Vitis vinifera genes encoding chitinases differentially expressed in berries and leaves infected beningal or bacterial pathogens.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ291506; CAC14015.1; -.

InterPro; IPR001022; Chitin.bind.

InterPro; IPR001022; Chitin.bind.

Pfam; PF00182; Glyco_hydro_19.

Pfam; PF00182; Glyco_hydro_19; 1.

Pfam; PF00182; Glyco_hydro_19; 1.

Probom; PD000574; Glyco_hydro_19; 1.

Probom; PD000574; Glyco_hydro_19; 1.

SMART; SM00270; ChtBDI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 YFGRGPIQISHNYNYGPCGRAIGVDLINNPDLVATDPVISFKSALWFWMTPQSPKPSCHD
                                                                                                                                                                                                                                                                            187 YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD
                                                                                                                                                                                                                                                            8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STASUE=LEAF;
STRANH=CV. UGNI BLANC; TISSUE=LEAF;
RODETT N., Roche K., Lebeau Y., Breda C., Boulay M., Esnault Buffard D.;
                                                                                                                                                                                                   Length 328;
                                                                                                                                                                                                                              Indels
                                                                                                                                                      328 AA; 35300 MW; F687A32555D9DB55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNA-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                               Query Match 71.4%; Score 1260; DB 10; Best Local Similarity 71.8%; Pred. No. 4.3e-103; Matches 224; Conservative 31; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 AA.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHTINBINDNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
SMARY; SM00270; ChtBD1; 1.
PROSITE; PS00773; CHTINASE_19_1; 1.
PROSITE; PS00774; CHTINASE_19_2; 1.
PROSITE; PS00774; CHTINASE_19_2; 1.
CHILIn-binding, RSQUENCE 328 AA; 35300 MW; F687A325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 GDNLDCYNQRPF 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=29760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9FS45;
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                                                                         CHITINASE. 05DE2B9575ABEAD8 CRC64;
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68.5%; Pred. No. 9.5e-103;
ive 41; Mismatches 48;
PROSITE; PSO0026; CHITIN_BINDING; 1.
Chitin-binding; Glycosidase; Hydrolase; PGGNAL
1 22 POTENTIAL.
CHAIN
SEQUENCE 325 AA; 34631 MW; 05DE2B957.
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CDLMGIGYGSNLDCNNQRPFS 325
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Run

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(without alignments)
3187.393 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (bases: Tro 1028)
Bryngelsson, T., Collinge, D.B., Green, B., Gummesson, P.O., Kragh, K. and Ihordal-Christensen, H. AF280438 Secale ce AJ276226 Hordeum v AB01647 Oryza sat AF001500 Oryza sat L40338 Oryza sativ X56787 O.sativa L. L37289 Oryza sativ AF000906 For prace X76041 Transtrum 184465 Sequence 2 D16223 Rice Cht-3 AP0013685 Oryza sat L34211 Hordeum vul M62904 H.vulgare E AR037574 Sequence 9 AR037574 Sequence 9 AR020964 For prace AF000964 For prace AF001513 Secale Ce AF000964 For prace AF001518 Secale Ce AF000966 Oryza sativ X55665 Oryza sativ X5467 Oryza sativ X5487 Oryza sativ X5487 Oryza sativ X5496 Oryza sativ X67109 O.sativa R7 AF01386 Oryza sat X87109 O.sativa R7 AR01386 Oryza sat X87109 Sequence AR027131 Sequence AR027131 Sequence AR067485 Sequence 107381 Sequence 7194437 Sequence 7194437 Sequence 7184437 Sequence 7184447 Sequence 7184447 Sequence 7184447 Sequence 71844476466 Sequence 7184447666 Sequence 7184447666 Sequence 7184447666 Sequence 7184447666 Sequence 71 X78671 H.vulgare m X78672 H.vulgare m AF000965 Poa prate 01-NOV-1994 Purification, characterization and cDNA sequence of a basic chitinase from barely infected with powdery mildew Unpublished 2 (bases 1 to 1028) PLN ALIGNMENTS HVCHT2A 1028 bp mRNA H.vulgare mRNA for chitinase 2a. X78671 HVCHT2B HVCHT2B AF280438 HVU276226 AB016497 OSAF001500 BLYCH126A AF280437 TACHIG 184465 RICCHT3 AP003685 BLYCHI33A RICCHITA AF000965 AF000966 BLYCHI A37990 AR037574 I75200 AB051579 AF000964 AC051633 OSENDO AB051578 HVU02287 OSCHIT AB012855 AB018248 AF013580 OSDNARC24 AR038418 AR064560 AR067485 I07381 OSLMRNAC AR020808 RICRCH0 I38437 GI:563486 DB 998 10002 10002 110002 11002 11002 11002 1102 1102 1102 1102 1102 1102 1102 1102 1102 1102 1102 1102 2 (bases Bryngelsson, T.L. 1291 1173 1080 1985 1151 141534 Length Hordeum vulgare X78671.1 G Query Match barley. 222995 222995 222995 223995 636.8 559.6 474.4 395.2 329.6 307.2 302.8 302.2 301.4 300.6 296.2 296 DEFINITION ORGANISM JOURNAL REFERENCE AUTHORS ACCESSION AUTHORS VERSION KEYWORDS SOURCE REFERENCE RESULT HVCHT2A TITLE しににしているのとととととととととととととととととととしてととしてしてことにしてられるようなもんととにしてもととしてもられるようなもんできることもといってもられるようなもとしてももとしているもんできる Result No.

01-NOV-1994

658 99

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Submitted (16-MAR-1994) T.L. Bryngelsson, Department of Plant
Breeding Research, The Swedish University of Agricultural Sciences,
S-268 31 Svaloev, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1013)
Bryngelsson, T., Collinge, D.B., Green, B., Gummesson, P.O., Kragh, K. and Thordal-Christensen, H. Purification, characterization and cDNA sequence of a basic chitinase from barely infected with powdery mildew
                               539 GIGTCCTTCAGGACGCCGAIGTGGGTTCTGGATGACGGCGCAGGGCAACAAGCCGTCGAGC
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2 (bases 1 to 1013)
Bryngelsson,T.L.
Direct Submission
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VSFFTAMWFWHTAQGVRFSSHNVALRWTPTAADIFAAGRVPGTGVTNIINGGLECGM
GRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFAS"
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/cultivar="Pallas, near-isogenic line P02"
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Pred. No. 9.4e-88;
0; Mismatches 37;
                Submitted (16-MAR-1994) T.L. Bryngelsson,
Breeding Research, The Swedish University
S-268 31 Svaloev, SWEDEN
Location/Qualifiers
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precursor, mRNA, complete cds.
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Yeh,S., Moffatt,B., Griffith,M., Xiong,F., Yang,D.S.C.,
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Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Secale.
                          Length 1013;
                                                                   Indels
                            659; DB 8;
No. 1.3e-80;
                                                                     0; Mismatches
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93.2%;
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ABLAKT OF THE TALGAGGS 610.1"

ABLAKT OF THE TALGAGGS 610.1"

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   Hew, C.L.
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                                                                                                                                                                                                         Tobases 1 to 998)
Yeh,S., Moffatt,B., Griffith,M., Xiong,F. and Hew Direct Submission
Submitted (20-UNN-2000) Biology, University of Wai University Ave West, Waterloo, ON NZL 361, Canada
Sarhan, F., Danyluk, J., Xue, Y.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.9%; Score 654.2; DB 8;
92.8%; Pred. No. 6e-80;
iive 0; Mismatches 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                      1. 998
/organism="Secale cereale"
/variety="Musketeer"
/db_xref="taxon:4550"
/chromosome="1"
                                Doherty-Kirby, A. and Lajoie, G. Chitinase genes responsive to cold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="24.8 kDa class
protein precursor"
                                                                                                             winter cereals
Plant Physiol. 124 (3), 1251-1264
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Itoh,Y., Yamamoto,K. and Sasaki,T.
Direct Submission
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                                                                                                                                                                                                                  HVU276226 890 bp mRNA PLN 16-AUG-2000
Hordeum vulgare mRNA for chitinase II (pathogenesis-related protein 3) (cht2 gene).
AJ276226
AJ276226.1 GI:9501333
Chitinase; cht2 gene; pathogenesis-related protein 3.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
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Submitted (20-JUL-2000) M. Bevan, John Innes Centre, Norwich, NR4
7UH, United Kingdom
                                                                                                                                                                                                                                                                                                                                                                                                    Isolation and characterisation of genes induced in barley during powdery mildew infection Unpublished
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                                                       ggccgccgacaccgctgccggcagggtacccggatacggaggtgatcaccaatatcatcaa
          cggcgggctcgagtgcggaatgggccggaacgacgccaacgtcgaccgcatcggctacta
                                                                                        cacgogotactgoggcatgotcggcacggcaccggaggcaacctcgactgotacaccca
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/organism="Hordeum vulgare"
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/country="United Kingdom"
/dev_stage="leaf"
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71..820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="cht2"
/function="endochitinase"
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/db_xref="GI:9501334"
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Green, R.M. and Bevan, M.
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                                                                                                                                       gaggaacttcgctagctag 771
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71. .820
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Green, R.M.
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Best Local Similarity
Matches 682; Conserv
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HVU276226
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Embryophyta; Tracheophyta;
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                   140
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ccagagggttctacacgtacgacgccttcatcgccgccgccaacaccttcccgggcttcg
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OLYZA SALiva mRNA for chitinase, complete cds.
AB016497.
AB016497. GI:3370779
Chitinase: chitinase IIa.
OLYZA SALiva
OLYZA SALiva
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzea.
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618 657

597

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Yun, C.-H., Lee, M.-C., Lee, J.S., Yun, K.J. and Eun, M.Y.
Direct Submission
Submitted (29-APR-1997) Dept.of Cytogenetics, National Institute of
Agricultural Science and Technology, RDA, Seodundong, Suweon
441-707, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="DDDDGEVCSACRVPAALLAVAAWRRQGVGSVITQAVFNSMLPNR
DNSQCPATGFYTSSAFIAAANSFRRSARAGAAPSSSRRELAAFFGQTSHETTGGTRGS
SDQFWGYCYCKEEINKATSPPYYGRGPIQLTGGSNYQAAGNALGLDLVGNPDLVSTDA
VVSRKTAIWFWATAGGNKASCHDVILGKWTRPGGEFTAGRVPGYGVITNIINGGIEGG
VGQNDANVDRIGYTKRYCDMLGTGYGSNLDCYNQRNLPAS"
                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza,
I (bases 1 to 913)
Yun, C.-H., Lee, M.-C., Lee, J.S., Yun, K.J. and Eun, M.Y.
Isolation and characterization of a rice chitinase cDNA clone from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGCG-----GCGGCAGGCGTCGGTCATCACGCAGGCGGTTTCAACAGCAT 121
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Cryza sativa clone MIRCH1 chitinase mRNA, partial cds.
AF001500
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                                                                                   538 tgccacaacgtcgccctacgccgctggacgccgacggccgccgacaccgctgccggcagg
                                                                                                                                   cggaacgacgccaacgtcgaccgcatcggctactacacgcgctactgcggcatgctcggc
                                                                                                                                                  559 IGCCACGACGTCATCCTCGGCCGGTGGACGCCGTCGGCGGCGGCGGAACACGCCGCCGCCGC
                                                                   598 gtacccggatacggagtgatcaccaatatcatcaacggcgggctcgagtgcggaatgggc
                                                                                                                                                                                                                 739 GCAGGCTACGGCAGCAACCTCGACTGCTACCAACCGAGCGCAACTTCGCCAGCTAG 792
                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="seedling"
/tissue_type="blast fungus-infected leaves"
/clone="MIRCH1"
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Pred. No. 1.4e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAB58238.1"
/db_xref="GI:2109455"
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79.2%;
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STDAVVSFKTAIWFWMTAQGNKPSCHDVILGRWTPSAAEHAAGRVPGYGVITNIINGG
IECGYGQNDANVDRIGYYKRYCDMLGAGYGSNLDCYNQRNFAS"
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                                                                                                                                                                                                                                                                                                /translation="MTTTTTRFVQLAACAAASLLAVAASGAAAQGVGSVITQAVFNSM
LPNRDNSQCPARGFYTYDAFIAAANSFPAFGTSGGSAELIRRELAAFFGQTSHETTGG
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2 (bases 1 to 923)
Itch,Y., Yamamoto,K. and Sasaki,F.
Nucleotide sequence of rice acidic class II chiitinase OsChia2a
Published Only in Database (1998) In press
Location/Qualifiers
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                                                                                                                                                                                                                                                /product="chitinase"
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                                                                                 1. .923
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/db_xref="taxon:4530"
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903. .908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="19 a nucleotides"
294 c 277 g 16
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                                                                                                                                                                            /gene="Rcht2"
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CDS //note="(vector lambda ZAPII)" (1.528 /Ec.number="3.2.1.14" /note="putative" /codon_start=1 /product="chitinase" /protein_id="AaA7516.1" /db_xxef="G1:2340043" /translation="ELAAF807SHETTGGTRGSSDQFOWGYCFKEEINKATSPPYG //translation="ELAAF807SHETTGGTRGSSDQFOWGYCFKEEINKATSPPYG //translation="ELAAF807SHETTGGTRGSSDQFOWGYCFKEEINKATSPPYG //translation="ELAAF807SHETTGGTRGSSDQFOWGYCFKEEINKATSPPYG //translation="ELAAF807SHETTGGTRGSSDQFOWGYCFKEEINKATSPPYG //translation="ELAAF807SHTAINFWHTAGGNKFSCHDV //translation="ElaAF807SHTAINFWHTAGGNKFSCHDV //translation="ElaAF807SHTAINFWHTAGGNKFSCHDV //translation="ElaAF807SHTAINFWHTAGGNKFSCHDV //translation="ElaAF807SHTAINFWHTAGGNKFSCHDV //translation="ElaAF807SHTAINFWHTAGGNKFSCHDV //translation="ElaAF807SHTAINFWHTAGGNKFSCHDV //translation="ElaAF807SHTAINFWHTAGGNKFSCHDV //translation="ElaAF807SHTAINFWHTAGGNKFSCHDV //translation="ElaAF807SHTAINFWHTAGGNKFSCHDV" //translation="ElaAF807SHTAINFWHTAGNKFSCHDV" //translation="ElaAF807SHTAINFWHTAGNKFSCHDV" //translation="ElaAF807SHTAINFWHTAGNKFSCHDV" //translation="ElaAF807SHTAINFWHTAGNKFSCHDV" //translation="ElaAF807SHTAINFWHTAINFWHTAINFWHTAGNKFSCHDV" //translation="ElaAF807SHTAINFWHTAIN	Ouery Match Best Local Similarity 84.38; Pred. No. 8.68-45; Matches 445; Conservative 0; Mismatches 93; Inels 0; Gaps 0; A44 ganctegorgottectrogrogacococococococococococococococococococ
121 Ctgcccaaccgcgacaactcgctgtgcccgggccagaggttctacacgtacgaccttc 180	0y 358 coccascontactutgacogaccacteantgacogaccactacattcacagacct 417

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----gocacgtccccaccatactatggacggggacccatccaattgacagggcggtc 404
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/db_xref="GI:561873"
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/organism="Oryza sativa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="seedling"
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IGYDLLSNPDLVATDATVSFKTALMFWMTPQGNKPSSHDVITGRWAPSPADAAAGRAP
GYGVITNIVNGGLECGHGPDDRVANRIGFYQRYGGAFGIGTGGNLDCYNQRPFNSGSS
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LHRNDGACPARGFYTYEAFLAAAAFPAFGGTGNTETRKREVAAFLGQTSHETTGGWP
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                                                                                                                                                                                                                                                                                                                                              /translation="MSTPRAASLAKKAALVALAVLAAALATAARAEQCGAQAGGARC
                                                                          Direct Submission
Submitted (13-NOV-1990) Y. Nishizawa, NATIONAL INSTITUTE OF
AGROBIOLOGICAL RESOURCES, TSUKUBA SCIENCE CITY, KANNONDAI, IBARAKI
305, JAPAN
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Mol. Gen. Genet. 241 (1-2), 1-10 (1993)
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                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                          /organism="Oryza sativa"
                                                                                                                                                                       /strain="japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
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/EC_number="3,2.1.14"
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/note="cysteine-rich
1050. .1055
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10, .1032
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106. .228
                                                                                                                                 Location/Qualifiers
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ITNIINGLECGFGPDDRVANRIGFYQRYCDVLGIGYGSNLDCYDQRPFNSGLAAVQ"
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Oryza sativa
Dryza sativa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhattoideae; Oryzeae; Oryza.
1 (bases 1 to 1291)
Yun, C.-H., Kim, J.-K. and Park, Y.-H.
Isolation and Characterization of A Rice Chitinase CDNA
Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                       818
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                                                                                          aaacaagccgtcgtgccacaacgtcgccctacgccgctggacgccgacggccgccgacac
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Oryza sativa chitinase mRNA, complete cds.
1.37289
1.37289.1 GI:561872
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/BC_umber="3.2.1.14"
/Function="chitinolytic activity, antifungal activity"
/evidence=experimental
/product="chitinase"
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21; Conservative
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(Chi3) pseudogene sequence.
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7. 1173
/organism="Poa pratensis"
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/db_xxef="taxon:4545"
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Liao, Y.C., Kreuzaler, F., Fischer, R., Reisener, H.J. and Tiburzy, R., Characterizatorn of a wheat class Ib chitinase gene differentially induced in isogenic lines by infection with Puccinia graminis Plant Sci. 103, 177-187 (1994)

Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 1985)
                      347 ACAACGCCTICATCGCCGCCGCCAACTCTTTCGCCGTTTCGGGACCACGGGCAGCACCG 406
                                                                                              ---ggacgagaggcgctgccgaccagttccagtggggctactgcttcaaggaagataa 346
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/organism="Triticum aestivum"
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71. .1595
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CHI gene; endochitinase.
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GTTSDYCGFGCQSQCNGCSGPTPVTPPSGGGGVSSIVSQSLFEDQMLLHRNDAACLAK
GTTSDYCGFGCQSQCNGCSGPTPVTPPSGGGGVSSIVSQSLFEDQMLLHRNDAACLAK
GFYTYNNETAANSFAGFGTTGSTDVRKREVAAFLAQTSHFTTGGWPTAPDGPVSWGY
CFKQEQGATSDYCSPSGWFCAPGKFYFGRPLOGSSNAVVGPAGQAIQTDLLNNPDL
VAIDPTVSFKTALMWFWATAQSFKPSSHAVITGQWSPSSADQAAGRVPGYGVITNING
GLECGGGQDNRVADRIGFYKRYCDLLGVSTGNNLDCXSQRPFGS"
366 c 327 g 179 t
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Submitted (22-APR-1997) Plant Biology,
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/db_xref="G1:6164588"
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Pred. No. 2.6e-32;
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554 c 552 g 412
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                                                                                               /gene="CHI"
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390. .394
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Zhu,Q. and Lamb,C.J.
Plant defense genes and plant defense regulatory
Patent: US 5695939-A 2 09-DEC-1997;
Location/Qualifiers aagegegacetegeegtetteggeeagaceteeeacgagaecaceggag Indels PAT 214; DB 6; 39.0%; Score 300.6; DB 6 llarity 65.6%; Pred. No. 4.3e-32; Conservative 0; Mismatches 214 cggaggcaacctcgactgctacacccagaggaacttcgc ų

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sig_peptide
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Matches 483;
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acggecatgtggttctggatgacggcgcagggaaacaagccgtcgtgccacaacgtcgcc
                                                                            1 (bases 1 to 2808)
Nishizawa,Y., Kishimoto,N., Saito,A. and Hibi,T.
Sequence variation, differential expression and chromosomal location of rice chitinase genes
Mol. Gen. Genet. 241 (1-2), 1-10 (1993)
               ctacgeegetggaegeegaeggeegeegaeaeegetgeeggeagggtaeeeggataegga
                                                                                                      613 gigalcaccaalalcalcaacggcgggctcgagtgcggaalgggccggaacgccaac
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Enrhartoideae, Oryzeae, Oryza.
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endochitinase.
Oryza sativa (strain Nipponbare) DNA, clone RCG3.
Oryza sativa
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1833. .2795
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Tsukuba, Ibaraki 305
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Nishizawa,Y.
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Saski,T., Matsumoto,T. and Yamamoto,K.

All Submission

All Submission

All Submission

Agrobiological Resources, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

7-1-13, Tsukuba, Ibaraki 305-8602, Japan

8-1-12, Tsukuba, Ibaraki 305-8602, Japan

8-1-12, Tsukuba, Ibaraki 305-8602, Japan

9-1-12, Tsukuba, Ibaraki 305-8602, Japan

9-
                                                                                                                                                                                                                   Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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, *** SEQUENCING IN
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
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      AP003685 141534 bp DNA
Oryza sativa chromosome 6 clone P0548E04,
PROGRESS ***, in ordered pieces.
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Pred. No. 1.8e-32;
0; Mismatches 203;
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/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
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AP003685.1 GI:14192855
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Best Local Similarity 66.1%;
Matches 483; Conservative
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                                               ccagacctagtgtccacggacgcggtggtgtccttcaggacggccatgtggttctggatg
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Search completed: May 3, 2002, 15:34:10 Job time: 4339 sec

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3, 2002, 14:36:06 ; Search time 309.71 Seconds (without alignments) 2134.247 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

0		Description	Rye chitinase-like	cDNA encoding a ma	cDNA encoding a ma	RCH10 chitinase ge	Rice chitinase RCH	Rye chitinase-like	Nucleotide sequenc	Sequence encoding	Floral organ-speci	cDNA encoding a ma	PR-Q cDNA cloned i
SUPERFERE		a	AAX24890	AAA96231	AAA96230	AAQ31408	AAQ81346	AAX24889	AAF54983	AAQ62518	AAV49982	AAA96224	AAQ06185
			20	21	21	13	16	20	22	15	19	21	11
		Query Match Length DB	756	1013	1077	1151	1151	954	3035	1002	1318	1163	1010
	æ	Query Match	84.5	61.0	42.5	39.0	39.0	38.8	38.6	38.3	34.0	31.9	31.1
		Score	651.2	470.6	327.4	300.6	300.6	299.4	297.4	295.6	262.2	246	239.6
		Result No.		1 (7)	9	4	5	9	7	œ	6	10	11

Tobacco PR-Q gene.	co PR-Q	0	Petunia extracellu			PR-P cDNA cloned i	Tobacco PR-P gene	PR-P protein encod	Sequence encoding	cDNA encoding a ma		Full length chitin	cDNA encoding a ma	Banana ripening fr	tomato	Wild tomato endoch	American elm chiti	8		Φ	Banana fruit ripen	Floral organ-speci	Sequence encoding	Endochitinase prec	Sequence of chimer	Sequence of chimer	Tomato-tobacco end	Potato infection i	Chitinase gene con	Basic chitinase ge	Banana fruit ripen	hitinas	cDNA encoding a ma
AAN90845	AAV62809	AAV72995	289	395	990	AAQ06186	281	AAV81601	AAQ05264	AAA96233		AAT79941	23	19	AAQ93034	103	AAT33325	AAQ12898	AAT89952	AAA58910	AAV69461	AAV49983	AAQ21007	AAQ68352	AAQ21193	AAQ21191	126	AAA40411	AA011093	4	946	AAX24892	523
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	239.6																	159	159	159	20	10	m	135.6	m	~	m	N	S	i	129	N	119.8
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ALIGNMENTS

BP.

AAX24890 standard; cDNA; 756

AAX24890

AAX24890;

CHT46; chitinase-like protein; antifreeze protein; AFP; winter rye; antifungal; fungicide; cold tolerance; frost tolerance; transgenic plant; preservation; cryopreservation; tumour; therapy; /*tag= a /note= "separately claimed in Claim 2" /note= "separately claimed in Claim 2" Rye chitinase-like protein CHT46 cDNA clone ch-46. Location/Qualifiers 1..756 /*tag= a 98WO-CA00745. 97US-0903872 d 21-JUN-1999 (first entry) /*tag= 6 67..756 /*tag= k 99. Secale cereale. 31-JUL-1998; W09906565-A2 31-JUL-1997; 11-FEB-1999. sig_peptide mat_peptide Key

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The present sequence encodes winter rye (Secale cereale L. cv. Muskateer) CHT46 preprotein (see AAW98081). Mature CHT46 (see AAW98081) is a chitinase-like protein that has chitinase (antifungal) and antifreeze activities. CHT46 cDNA (ch-46) was obtained by isolating pathogens or other stresses, i.e. under conditions when only chitinases with antifreeze activity would be expressed, and then sorting the cold-induced chitinase CDNAs to determine which encoded proteins with ice-binding ability. CHT46 and CHT9 (see AAW98079-80) have been cloned and expressed in bacterial and yeast (Pichia) systems and in Arabidopsis thaliana. The chitinase-like antifreeze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins can be used: to increase freezing tolerance of plants and microorganisms; to increase field survival of plants, animals and microorganisms exposed to sub-zero temperatures; to inhibit ice recrystallisation in biological materials or foods; for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases or spoilage caused by low temperature pathogens (particularly fungi) in plants, frozen foods and any cryopreserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cryopreservation and hypothermic protection of calls, embrycs, tissues etc. (particularly human platelets); and to kill tumour cells. They are also used to inhibit initiation and progression
                                                                                                                                                                 New nucleic acid encoding antifreeze polypeptides from plants -
particularly with chitinase activity, used to impart frost, and
pathogen, resistant to plants, for preservation of foods, cells
                                                                                                                                                                                                                                                                                     Claim 2; Fig 22b; 118pp; English.
                                                                                                                           P-PSDB; AAW98081, AAW98082.
                                                                                                                                                                                                                                             and for treating tumours
              (ICEB-) ICE BIOTECH INC
                                                           нем С,
                                                                                                      WPI; 1999-153795/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biological material
                                                           Griffith M,
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etc.

Xiong F;

Moffatt B,

Sequence 756 BP; 140 A; 263 C; 237 G; 116 T; 0 other;

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; 0 392 452 512 201 caccaccygcaycacygacyacytcaaycycyayytcyccyccttcttcyyccayacetc 260 acacgagaccaccggagggactagaggcgccgaccgatccagttggggctactgctt 320 cateaegeagteeatgtaegegageatgetgeeeaaeegegaeaaetegetgtgeeegge 140 cateaegeggteggtgtaegegageaetetgeeeaacegegaeaaetegetgtgeeegge 152 Gaps 21 egecgegettettetegeegtggeggtgggeggegeegeggegegegeggggeteegt 80 caccacoggeagegecgacgacateaagegegacctegecgecttetteggecagacete ccacgagaccaccggagggacgagaggcgctgccgaccagttccagtggggctactgctt caaggaagagataagcaaggccacgtccccaccatactaggacggggacccatccaatt gacagggcggtccaactacgatcttgccgggagagcgatcgggaaggacctggtgagcaa gacagggcggtccaactacgatctcgccgggagagccatcgggaaggacctggtgagcaa cccagacctagtgtccacggacgcggtggtgtccttcaggacggccatgtggttctggat cagagggttctacacgtacgacgccttcatcgccgccgacacaccttcccggggcttcgg ; 0 Length 756; Indels Score 651.2; DB 20; Pred. No. 1.2e-105; 53; 0; Mismatches 84.5%; 92.8%; 683; Conservative Similarity Query Match 261 321 381 453 213 333 393 Matches 6 153 33 81 qq qq δŏ Db ØΫ δŏ qq ď g δŏ g qq δğ ò ŏ

The present sequence encodes a chitinase polypeptide. The specification describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896, AAB18895, and AAB18902-05), and glucosyl hydrolase family 18 chitinases (AAB18895, AAB18897-98 and AAB18900-01). The level of chitinase in plants can be modulated to enhance disease resistance in crop plants and for control of pathogens. The chitinase polynucleotides are also useful as molecular markers for genotype in a plant, and for sequence shuffling. maize chitinase genes encoding seven chitinases of glucosyl colase family 19 are useful for enhancing disease resistance in crop 18; 620 692 752 681 cacacgctactgcggcatgcttggcacggccaccggggggcaacctcgactgctacaccca 740 cccggacctggtgtccacggacgcggtggtttccttcaggacggccatgtggttctggat 500 Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase famiy pathogen control; disease resistance; molecular marker; ss. gotgecgataaegetgegggtegggteeetgggtaeggegtaateaecaatateateaa ggeegacacegetgeeggeagggtaceeggatacggagtgattaceaatateateaa cacgogetactgcgggcatgctcgggcacgggggggggggggaacctcgactgctacaccga cggcgggctcgagtgcggaatgggccggaacgacgccaacgtcgaccgcatcggctacta cDNA encoding a maize chitinase polypeptide designated 2mCh15 hydrolase family 19 are useful for enhancing d plants by modulating its expression in plants /product= "chitinase" Location/Qualifiers Claim 1; Page 84-85; 96pp; English. AAA96231 standard; cDNA; 1013 BP. (PION-) PIONEER HI-BRED INT INC. 99US-0125915. 2000WO-US06121 (first entry) ø gaggaacttcgctagc 768 741 gegaaacttegetage 756 75..833 Yalpani N; /*tag= WPI; 2000-628269/60 P-PSDB; AAB18903 WO200056908-A2 09-MAR-2000; 24-MAR-1999; Simmons CR, 08-FEB-2001 28-SEP-2000 AAA96231; Zea mays. 753 441 501 573 561 633 621 693 g qq δŽ qq δğ ŏ q ð

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                                        Length 1013;
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           G; 190 T; 0 other;
                                        DB 21;
                                                             144;
                                       Score 470.6; DB 21
Pred. No. 3.8e-74;
0; Mismatches 144;
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79.5%;
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                                         Query Match
Best Local Similarity
           BP;
           Sequence 1013
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The present sequence encodes a chitinase polypeptide. The specification describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896, AAB18895, AAB18897-98 and AAB1800-01). The level of Chitinases (AAB18895, AAB18897-98 and AAB1800-01). The level of Chitinase plants can be modulated to enhance disease resistance in crop plants and for control of pathogens. The chitinase polynucleotides are also useful as molecular markers for genotype in a plant, and for sequence
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Pred. No. 3.7e-49;
0; Mismatches 246;
                  "chitinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 82-83; 96pp; English.
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Best Local Similarity 66.5
Matches 501; Conservative
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                                                               WO200056908-A2
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           tacgccgctggacgccgacggccgccgccgccggcagggtacccggatacggag
                                                                 ccggcgcctggacgccgtccgccaccgaccgcgccgcgggagggtcccgggatatggcc
                                                                                        tgatcaccaatatcatcaacggcgggctcgagtgcggaatgggccgg---aacgacgcca
                                                                                                   acgtcgaccgcatcggctactacacgcgctactgcggcatgctcggcacggccaccggag
                                                                                                                                                          ccaaggaccgggtcggctactacaagaggtactgcgatatgctccgggtggggtacgggg
                                                                                                                                                                                                                                                                                                                                                   Promoter; region; rice; chitinase; physical; biological; stress; leaves; stems; roots; male; female; reporter; monocotyledon; dicotyledon; development; plant; defence; selectable; genes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LUMN LEAGMENT CONTG. Chitinase gene and its regulatory region responsive to mature plant stress and has low level expression leaves, moderate level expression in stem and high level expression in roots
                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
1053..1058
/*tag= b
/nota= "Putative polyadenylation signal"
1093..1098
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/note= "putative polyadenylation signal"
422..1021
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55..1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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The sequence given represents the rice chitinase gene. The promoter region of this gene (see AAQ31407) is responsive to physical and/or biological stress. The pattern of expression of this gene in mature plants is characteristic. There is a low level of expression in leaves, a moderate level in plant stems and the highest level in roots and the male and female parts of the plant. The chitinase promoter sequence may be linked to a reporter gene for expression in mono- or dicotyledon plants. Expression of this reporter gene may be used to study patterns of development and controlled expression of plant
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                                                                                                                                                                                                                                                                                                                                                                Transgenic plants contg. several plant defence associated proteins - have increased resistance to plant pathogens when
                                                                                     Chitinase; RCH10 gene; transgenic plant; disease resistance; crop improvement; tobacco; Nicotiana tabacum; plant defense; fungus pathogen; Cercospora nicotinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T; 0 other;
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                                            (first entry)
                                                                  Rice chitinase RCH10 gene.
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    AAQ81346 standard;
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                                                                                                                                           Oryza sativa.
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                                            13-AUG-1995
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The present sequence encodes winter rye (Secale cereale L. cv. Muskateer) CHT9 preprotein (see AAM98079). Mature CHT9 (see AAM98080) is a chitinase-like protein that has chitinase (antifungal) and antifreeze activities. CHT9 cDNA (ch-9) was obtained by isolating mRNA from rye plants grown at low temperatures in the absence of pathogens or other stresses, i.e. under conditions when only chitinases with antifreeze activity would be expressed, and then sorthing the cold-induced chitinase cDNAs to determine which encoded proteins with ice-binding ability. CHT9 and CHT46 (see AAM98081-82) have been cloned and expressed in bacterial and yeast (Pichia) systems and in Arabidopsis thallana. The chitinase-like antifreeze proteins can be used: to increase freezing tolerance of plants and microorganisms; to increase field survival of plants, animals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        microorganisms exposed to sub-zero temperatures; to inhibit ice recrystallisation in biological materials or foods; for cryopreservation and hypothermic protection of cells, embryos, tissues etc. (particularly human platelets); and to kill tumour cells. They are also used to inhibit initiation and progression of diseases or spoilage caused by low temperature pathogens (particularly fungi) in plants, frozen foods and any cryopreserved
                                                New nucleic acid encoding antifreeze polypeptides from plants particularly with chitinase activity, used to impart frost, and pathogen, resistant to plants, for preservation of foods, cells
                                                                                                                                                                                    Claim 2; Fig 21a; 118pp; English.
P-PSDB; AAW98079, AAW98080.
                                                                                                                                   and for treating tumours
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Sequence 954 BP; 162 A; 335 C; 306 G; 151 T; 0 other;

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                               Gaps
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                               42;
 Length 954;
                               Indels
   DB 20;
           ,9e-44;
nes 221;
              Pred. No 2.9e
0; Mismatches
 Score 299.4;
Pred. No. 2.9
38.8%;
Local Similarity 65.3%;
hes 494; Conservative
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The present sequence encodes a chitinase designated RCH10. The specification describes chimeric receptors which are used for modulating plant responses to pathogens. The receptors comprise a heterologous extracellular domain (e.g. from a Bril protein or RCH10 protein) and a kinase domain (e.g. from disease resistance protein Xa21). The Xa21 gene is a member of disease resistance genes referred to as RKK genes. When Xa21 is present in a transgenic plant, it confers resistance to Xanthomoras spp. The plant receptors containing heterologous domains are useful for modulating plant responses to pathogens including viruses, bacteria, nematodes, fungi or insects. The nucleic acids can be used to confer desired traits on essentially any plant.
                                                                                                                                                                                                                                                                                                                                                                                                          Disease resistance protein; Xa21; RKK gene; transgenic plant; chitinase; Xanthomonas; plant pathogen; Bril protein; RCH10 protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric plant receptors comprising a polynucleotide encoding a RRK receptor containing a heterologous extracellular domain and a kinase domain from a Xa21 polypeptide, useful for modulating plant responses
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                    gtgtcgccgaaccgaatcgggttctacaagcgctactgtgacctcctcggcgtcagctacg
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/product= "chitinase RCH10"
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                                                                                                                                                                                                                                                                                       AAF54983 standard; DNA; 3035 BP
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/*tag= a
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P-PSDB; AAB67444.
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Hordeum vulgare
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                                                               sig_peptide
                                                                                 mat_peptide
                                                                                                                                                         21-APR-1994
                                                                                                                                                                                                                                          Mundy J,
                                                                                                                                                                                                                                 Chet I,
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                                                                                                             2326 aagogogaggtogoogogttoottgogoagacgtoccacgagaccaccggogggtgggog 2385
                                                                                                                                                                                                                                2386 acggcgcccgacggcccctacacgtggggctactgcttcaaggaggagaacggcggcgc 2445
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                                                                                                                                                                            294
                                                                                                                                       237
                                                               58 geggggggtgcegeggegeagggegtgggeteggteateaegeggteggtgtaegegage 117
                                             Gaps
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                                                                                                                                      178 ttcatcgccgccaacaccttcccgggcttcggcaccaccggcagcgcgacgacatc
                                                                                                                                                        --cccaccatactat
                                                                                                                                                                                                                                                                    2446 gggccggactactgccagcagagcgcgcagtggccgtgcgccggcaagaagtactac
                                                                                                                                                                                                                                                                                       373 ggacggggacccatccaattgacagggcggtccaactacgatcttgccgggagagcgatc
                                                                                                                                                                                                                                                                                                                            gggaaggacctggtgagcaacccagacctagtgtccacggacgcggtggtgtccttcagg
                                                                                                                                                                                                                                                                                                                                                                                                    ctacgccgctggacgccgacggccgccgacaccgctgccggcagggtacccggatacgga
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                                            45;
                         Length 3035;
                                   Pred. No. 5.9e-44;
0; Mismatches 216; Indels
G; 749 T; 0 other
                          22;
                           DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          733 aacctcgactgctacacccagaggaacttcgct 765
                           Score 297.4;
Pred. No. 5.96
Sequence 3035 BP; 715 A; 832 C; 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; cDNA; 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoding chitinase G.
                           38.6%;
65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                             Matches 492; Conservative
                          Query Match
Best Local Similarity
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This sequence encodes Chitinase G. Chitinase is an enzyme which breaks down chitin, the major protein in insect exoskeletons. The coding sequence may be used in the construction of transgenic organisms, especially plants, to produce pathogen resistant organisms. The genome of such transgenic organisms preferably contains more then one gene with pathogen inhibiting activity, each gene under the control of active promoters. The two gene products then show a synergistic increase in pathogen induced activity so that the transgenic organisms have a greater degree of resistance or resistance or adder spectrum of diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic organisms contg. at least 2 pathogen inhibiting genes - esp. plants contg. genes with antifungal activity, show synergistic increase in disease resistance, also new DNA transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
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/note= "Putative polyadenylation signal."
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Pred. No. 1.3e-43;
); Mismatches 244;
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                                                                                                                                   Chitinase
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                                                Location/Qualifiers
64..864
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Goernhardt B;
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Best Local Similarity 63.8%;
Matches 504; Conservative 0
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905..910
/*tag= d
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gogggatogagtgcggtcacggggcaggacagccgcgtcgccgatcgaatcgggtttttaca
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                                                                     ---aaggecacgtecccaccatactatggacggggacccatccaattga
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/product= "floral-organ specific chitinase"
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                             tecagtggggetactgetteaaggaagagataage
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114..1100
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                                                                                                                                   This cDNA encodes a floral organ-specific chitinase. The specification provides a promoter sequence (AAV49083) derived from rice associated with chitinase, specific to floral organs that allows expression of genes in the flower parts of monocotyledonous plants. The expression of desired genes specifically in the floral parts of monocotyledonous plants, allows modifications to be made in the structure or function of these parts allowing the introduction of desired characteristics such as increased resistance to bacterial attack.
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                               Promoter sequence associated with chitinase, specific to floral organs - allows expression of genes in the flower parts of monocotyledonous plants
                                                                                                                                                                                                                                                                                                                                                          Length 1318;
                                                                                                                                                                                                                                                                                                                                                                                            36;
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                                                                                                                                                                                                                                                                                                    Sequence 1318 BP; 231 A; 442 C; 440 G; 205 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                      Score 262.2; DB 19;
Pred. No. 8.7e-38;
0; Mismatches 253;
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                                                                                                     Claim 7; Pages 33-35; 67pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                        34.0%;
62.9%;
                                                                                                                                                                                                                                                                                                                                                                                          490; Conservative
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P-PSDB; AAW64776
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR-Q cDNA cloned into plasmid pBScht15
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Moyer MB;
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89US-0329018.
89US-0368672.
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20-JUN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New maize chitinase genes encoding seven chitinases of glucosyl hydrolase family 19 are useful for enhancing disease resistance in crop plants by modulating its expression in plants
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1014 ctcggctcggctaccggcccaacctggactgcttcggccaggcggcggtcggacggcga 1072
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                                                                                                                                                                                                                     Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase famiy 18; pathogen control; disease resistance; molecular marker; ss.
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                                                                                                                                                                                         cDNA encoding a maize chitinase polypeptide designated ZmCh7
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Pred. No. 5.9e-35;
0; Mismatches 225;
                                                                                                                                                                                                                                                                                                                                                  /product= "chitinase|
                                                                                                                                                                                                                                                                                         Location/Qualifiers 32..817
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                                                                                              ВP
                                                                                              CDNA; 1163
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62.5%;
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P-PSDB; AAB18896.
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466; Conserv
                                                                                           AAA96224 standard;
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24-JAN-1990
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Payne G;
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                                                                                                                                                                                                                        ggcacaaggcattggttctattgtaacgagtgacttgttcaacgagatgctgaagaatag 164
                                                                                                                                                                                 Gaps
                                                This chimeric DNA sequence comprises the PR-Q plant pathogenesis-
related protein (PRP)-coding sequence,(1), and a promoter sequence
which enhances transcription of (1). This construct is used to
produce transgenic plant cells or -tissues with the ability to re-
generate into plants which are disease resistant.
See also AAQ06179-84, AAQ06186, AAQ06199-Q06208 and AAQ06829.
                                                                                                                                                                                                                                          cgacaactcgctgtgcccggccagagggttctacacgtacgacgccttcatcgccgccgc
                                                                                                                                                                                                                                                      ggcgcagggcgtgggctcgtcacgcggtcggtgtacgcgagcactctgcccaaccg
                                                                                                                                                                                                                                                                                   caacacetteeegggetteggeaceaceggeageegaegaeateaagegegeetege
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                                                                                                                                                           Length 1010;
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 Disease-resistant transgenic plants - obtd. using encoding a inducible pathogenesis-related protein from infected plants.
                                                                                                                                                                               Indels
                                                                                                                         Sequence 1010 BP; 310 A; 178 C; 239 G; 283 T; 0 other;
                                                                                                                                                Score 239.6; DB 11;
Pred. No. 7.8e-34;
                                                                                                                                                          DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                               0;
                                                                                                                                                        31.1%;
illarity 61.3%;
Conservative
                             77pp;
                               17; page 26;
                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                            424;
                                                                                                                                                                              Matches
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RESULT 12
AAN90845
ID AAN90845 standard; cDNA; 1020
XX
AC AAN90845;

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and vectors
and insect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence is tobacco PR-Q gene ( PR = pathogenesis-related), cont. in plasmid BESCHIE. PR-Q is a chemically inducible gene used to regulate transcription of an associated DNA sequence in plant tissue. See also AAN90367, AAN90368, AAN90841-N90846, and AAP91383-P91386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191
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                                                                       herbicide resistance; pBScht15; transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 cgacaactcgctgtgcccggccagagggttctacacgtacgacgccttcatcgccgccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgggaaggacctggtgagcaacccagacctagtgtccacggacgcggtggtgtccttcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1020;
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                                                                                                                                                                                                                                                                                                                                                                Meins
                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence
to herbicide
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                                                                                                                                                                                                                                                                                                                                                                Sperisen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 239.6; DB Lv,
pred. No. 7.8e-34;
".hes 259; J
                                                                                                                                                                                                                                                                                                                                                                                                                 Chemical induction of cloned genes in plants - and processes for inducible expression leading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             Duesing J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 81; page 79; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                             Harms C,
                                                                                                         cv. Xanthi
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61.3%;
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   entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                of
                                                                                                                                                                                                                                                                                       GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                               Montoya A,
(first
                                                                                                                                                                                                                                                                                                                         WPI; 1989-265342/37
                                                                                                       Nicotiana tabaccum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                       Tobacco PR-Q gene;
                                                                                                                                                                                                                                                                                                                                                                                                              Chemical induction
                                     gene
                                   Tobacco PR-Q
                                                                                                                                                                                                                                                                                       (CIBA ) CIBA
                                                                                                                                                                                                                 06-MAR-1989;
                                                                                                                                                                                                                                                   08-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424;
                                                                                                                                                                               13-SEP-1989
                                                                                                                                         EP332104-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a clone of the tobacco pathogenesis related (PR)

gene. This gene can be isolated using the method of the invention.

The method is for isolating a chemically regulatable DNA promoter

fragment from the 5' flanking region of a chemically regulatable gene in

fragment from the controlled expression of genes, under the control of a

consecul for the controlled expression of genes, under the control of a

con-coding regulatable sequence. This is useful in plants with a

connecoding regulatable sequence. This is useful in plants with a

connecoding regulatable sequence. This is useful in plants with the

conformator. The regulatator being applied before or with the

cherbicide or pesticide to give optimal tolerance. The promoter fragment

conformation for development, make or female sterility, and the ability

cof the plant to withstand cold, heat, salt and drought. The chemical

induction of the promoter allows the regulation of production of

compounds, es, flavours, fragrances, pigments, natural sweeteners,

industrial feedstocks, antimicrobials and pharmaceuticals, by

compounds, es, flavours, fragrances, pigments, or industrial feedstocks, antimicrobials and pharmaceuticals, by

confounds, es, controlling sens. The method allows control over the time

conditions or foreign genes. The method allows control over the time

and rate of gene expression either throughout the whole plant, or in

conditions the leaves with the chemical regulator. Controlling the

controlling the leaves with the chemical regulator.
             611
                                                                                                                                                                     696 ggaagatcgaattggatactacaggaggtattgtggtatgttaaatgttgctccgggggga 755
                                                                                                      636 tgtaattaccaacatcattaacggtggaattgaatgtggcataggacggaatgacgcagt 695
                                                                                                                                                                                                                                                                                                                                                                                                                                             pesticide;
                                                                        agtgatcaccaatatcatcaacggcgggctcgagtgcggaatgggccggaacgacgccaa
                                                                                                                                     cgtcgaccgcatcggctactacacgcgctactgcggcatgctcggcacggccaccggagg
             cetacyccyctygacyccyacygccyacyccyacaccyctyccyycayyytacccyyatacyy
                                        categgtegttggaeteegtetgeegeggateaggeggaategagtaeegg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolating chemically regulatable DNA sequences in plants - useful for chemically controlling expression in transformed plants
                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemically regulatable DNA promoter; expression control; herbicide tolerance; pathogenesis related gene; PR gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 46; Column 177-180; 175pp; English.
                                                                                                                                                                                                     763
                                                                                                                                                                                                                    732 caacctcgactgctacacccagaggaacttcg
                                                                                                                                                                                                                                                                                                                  ВР
                                                                                                                                                                                                                                                                                                                 AAV62809 standard; cDNA; 1020
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                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            Tobacco PR-Q gene clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana acuminata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-080396/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ryals JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAY-1995;
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developmental processes by the application of a regulating chemical in e.g. the commercial production of cultivated crops allows processes such as germination, flower formation and fruit ripening to be synchronised at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tggacggggacccatccaattgacagggcggtccaactacgatctgccgggagagcgat 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 tggacaagagctagttaacaaccctgatttagtggccacagatgctactatatcattcaa 515
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                                                                                                                                                                                                                                                                                                                                                 72 ggcgcagggcgtgggctcggtcatcacgcggtcggtgtacgcgagcactctgcccaaccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 gaacgacggtagatgteetgeeaatggettetacaettatgatgeatteatagetgetge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 tgcctttttcggtcaaacttctcacgaaactactggtggatccctgagtgcag--aacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343 tttacaggaggtattgctttgttaggcaaaatgaccagagtgac----agatetta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636 tgtaattaccaacatcattaacggtggaattgaatgtggcataggacggaatgacgcagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 egecttetteggeeagaeeteeeaegagaeeaeggaggaeggaggagggegetgeegaeea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 cetacgecgetggacgecgacggecgecgecgecgetgeeggcagggtaeeeggataegg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caacaccttcccgggcttcggcaccaccggcagcgacgacgacatcaagcgcgacctcgc
                                                                                                                                                                                                                                   DB 20; Length 1020;
                                                                                                                                                                                                                                                                                          6
                                                                                                                                           Sequence 1020 BP; 310 A; 181 C; 240 G; 289 T; 0 other
                                                                                                                                                                                                                          Score 239.6; DB 20;
Pred. No. 7.8e-34;
0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR-Q protein encoding cDNA sequence.
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                                                                                                                                                                                                                                31.1%;
61.3%;
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                                                                                                                                                                                                                                                         Best Local Similarity 61.3
Matches 424; Conservative
                                                                                        a given time.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-1999
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                                                                                                                                                                                                                                   Query Match
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ID AAV7
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431

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ogggaaggacctggtgagcaacccagacctagtgtccacggacgcggtggtgtccttcag 491
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                                                                                tggtagaggacccatccaattgacaaaccgaaataactatgagaaagctggaactgcaat
                                                                                                                                           456 tggacaagagctagttaacaaccutgatttagtggccacagatgctactatatcattcaa
                                                                                                                                                                            gacggccatgtggttctggatgacggcgcagggaaacaagccgtcgtgccacaacgtcgc
                                                                                                                                                                                                                                                                                                   612 agtgatcaccaatatcatcaacggcgggctcgagtgcggaatggggcgggaacgaccaa
                                                 tggacgggggacccatccaattgacagggcggtccaactacgatcttgccgggagagcgat
                                                                                                                                                                                                                                                                                                                                                                 cgtcgaccgcatcggctactacacgcgctactgcggcatgctcggcacggccaccggagg
                                                                                                                                                                                                                                         cctacgccgctggacgccgacggccgccgacaccgctgccggcagggtacccggatacgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plants with improved resistance to pathogenic fungi - contains chitinase and/or beta-1,3-glucanase genes modified for over-expression targetted to apoplasts
   Van
Bol
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Woloshuk CP,
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                                                                                                                                                                                                                                                                                                                                                                                                                           732 caacctogactgotacaccoagaggaacttog 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                          trog
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25..93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resistance; phytopathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melchers LS, M
, Vloemans AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ12897 standard; cDNA; 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOGE-) MOGEN INT NV.
(UYLE-) RIJKSUNIV TE LEIDEN.
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/product= e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR13274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cornelissen BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-0CT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 ggcacaaggcattggttctattgtaacgagtgacttgttcaacgagatgctgaagaatag 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding pathogenesis-related glucanase proteins – useful for producing transgenic plants with enhanced disease or pest resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 gaacgacggtagatgtcctgccaatggcttctacacttatgatgcattcatagctgctgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cgccttcttcggccagacctcccacgagaccaccggagggacgaggaggcgctgccgacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caacaccttcccgggcttcggcaccaccggcagcgccgacgacatcaagcgcgacctcgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 239.6; DB 20;
Pred. No. 7.8e-34;
); Mismatches 259;
beta-1,3-glucanase activity; pest resistance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 46; Column 171-174; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ward ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ryals JA,
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llarity 61.3%;
Conservative (
                                                                                                                                                     95US-0457364.
88US-0165667.
89US-0305566.
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90US-0580431.
90US-0632441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-059180/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                     31-MAY-1995;
08-MAR-1988;
06-FEB-1989;
                                                                                                                                                                                                                                                                                                         06-MAR-1992;
06-NOV-1992;
06-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                        16~JUL-1993;
13-JAN-1994;
                             Nicotiana sp
                                                                                                                                                                                                                                                                               01-APR-1991;
27-SEP-1991;
                                                                                                                         31-MAY-1995;
                                                                                                                                                                                                     24-MAR-1989;
                                                                                                                                                                                                                    20-JUN-1989;
                                                                                                                                                                                                                                                07-SEP-1990;
21-DEC-1990;
                                                           US5847258-A.
                                                                                                                                                                                                                                                                                                                                                            12-APR-1993;
                                                                                        08-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moyer MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424:
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Matches
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Roekel JS; JF:

Ωp δλ g Ö qq ŏ g δ

δλ

Example 4; Fig 1; 55pp; English

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                                                                                                                                                                                                                                                                              90 ggcacaaaatgiiggiictatigigacaagcgactiatiigaccagaigciiaaaaatag 149
                                                                                                                                                                                                                                                                                                              cgacaactcgctgtgcccggccagaggttctacacgtacgacgccttcatcgccgccgc 191
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                                                                                                                                                                                                                                                    72 ggcgcagggcgtgggctcggtcatcacgcggtcggtgtacgcgagcactctgcccaaccg 131
                                                                                                                                                                                                                         Gaps
                                  This sequence was isolated from a P.hybrida cDNA library. It has 80 per cent homology with tobacco clone PROB30 which encodes extracellular chitinase PR-Protein R. The gene can be inserted into an appropriate plasmid for production of transgenic plants having resistance to fungal pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447 tgaacaagacttagttaacaaccctgatttagtagcaacagatgctactgtatcattcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                507 aacagcaatatggttctggatgacaccacagggtaacaagccatcttgccacgacgttat
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                                                                                                                                                                                                                         3,
                                                                                                                                                                                           DB 12; Length 965;
                                                                                                                                                                                                                         Indels
                                                                                                                                              Sequence 965 BP; 300 A; 173 C; 218 G; 274 I; 0 other;
                                                                                                                                                                                        Query Match 30.5%; Score 235.4; DB 12; Best Local Similarity 59.7%; Pred. No. 4.2e-33; Matches 414; Conservative 0; Mismatches 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             caacctcgactgctacacccagaggaacttcgc 764
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CITY: Los Angeles
STATE: Callfornia
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TELEFAX: (619) 546-9392
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LENGTH: 1151 base pairs
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Patent No. 5399680
GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: ELEMENTS
UNMERR OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower street, Suite 2000
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: 22-MAY-1991
CLASSIFICATION: 800
ATTORNEY/AGANT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 300.6; DB 1;
Pred. No. 1.1e-51;
0; Mismatches 214;
ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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433
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                                                                         118 actotycocaaccycyacaactcyctytycocyycoayayyyttotacacytacyacycc
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APPLICANT: Lamb, Christopher J.
APPLICANT: Zhu, Qun
APPLICANT: Maher, Eileen A.
APPLICANT: DAO, Richard A.
TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING MULTIPLE
TITLE OF INVENTION: DISEASE RESISTANCE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    982 AACTTGGATTGCTACAGCCAGAGGCCTTCGGCT 1014
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Patent No. 5530187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 444 South
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 90071-2921
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US-08-093-372-1
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               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 300.6; DB 1;
Pred. No. 1.1e-51;
0; Mismatches 214;
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US-08-093-372-1
                                                                                    16-701.05/08/093,372
16-701.1993
18-800
18-701.05/093
                                                                                                                                            CLASSIFICATION.
ATTORNEY/AGENT INFORMATION.
NAME: Retler, Stephen 31,192
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 935
TELEPHONE: 619-546-437
TELEPHONE: 619-546-9392
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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65.6%;
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Best Local Similarity 65.6
Matches 494; Conservative
COMPUTER READABLE FORM:
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                                                                                                                                                                322 ATGCTGCTCCACCGCAACGATGCGGCGTGCCCGGCCAGCAACTTCTACACCTACGACGCC
                                                                        ttcatcgccgccgacacacttcccgggcttcggcaccaccggcagcgccgacgacatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond STREET: 30 Rockefeller Plaza CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New YOLK
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/08457797A Patent No. 5689045 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                   862 GICAICACCAACAICAICAACGCCGGGCIGGAGIGCGGCCAIGGCGAGGACGAICGCAIC
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                                                                                                                                                                                                                                                                                                                                            APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: BEFENSE REGULATORY
TITLE OF INVENTION: BLEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCES: 26
CORRESPONDENCES: 26
ADDRESSES: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REDABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.0%; Score 300.6; DB 1; 65.6%; Pred. No. 1.1e-51; iive 0; Mismatches 214;
                                                                                                                                                                                                   AACTIGGATIGCTACAGCCAGAGGCCTICGGCT 1014
                                                                                                                                                                aacctcgactgctacacccagaggaacttcgct 765
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TELECOMONULACHION INFORMATION:
TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08379259
Patent No. 5695939
GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1151 base pairs TYPE: nucleic acid
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Matches 494; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
: United States
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STREET: 444
CITY: LOS F
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US-08-379-259-2
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TITLE OF INVENTION: Tr. NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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US-08-812-025-9
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/function= "chitinase"
/product= "26 kD preprotein of chitinase G (ChiG)"
/note= "antifungal activity, especially on
Trichoderma reesli and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 862..1002
OCHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3' end not shown"
FEATURE:
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LOCATION: 905.310
OCHER INFORMATION: Anote= "potential polyadenylation
OTHER INFORMATION: signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: sig_peptide
LOCATUON: 298..312
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: sig_peptide
LOCATION: 466..588
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
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sequence"
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                          REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
TELECOMMONICATION INFORMATION:
TELEFAX: (212) 765-250
TELEFAX: (212) 765-259
TELEFAX: (212) 765-259
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.3%; Score 295.6; DB 1;
63.8%; Pred. No. 1e-50;
live 0; Mismatches 244;
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OTHER INFORMATION: /note= "p
OTHER INFORMATION: sequence"
FEATURE:
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OTHER INFORMATION: sequence"
18,839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: sig_peptide
LOCATION: 349..378
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133..861
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LOCATION: 607..861
OTHER INFORMATION: /nc
OTHER INFORMATION: Sev
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 REGISTRATION NUMBER:
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     LOCATION: 64..861
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
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OTHER INFORMATION:
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Best Local Similarity
Matches 504; Conserv
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NAME/KEY: 3'UTR
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LOCATION: 1..63
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; LOCATION:
US-08-457-797A-9
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                                                agggcgtgggctcggtcatcacgggtcggtgtacgcgagcactctgcccaaccgcgaca 136
                                                                                         GCAGCGTGTCCTCCATCGTCTCGCGCGCACAGTTTGACCGCATGCTTCTCCACCGCAACG 190
                                                                                                                                                  actcgctgtgcccggccagagggttctacacgtacgacgccttcatcgccgccgccaaca 196
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Patent No. 5804184
GENERAL INFORMATION:
APPLICANT:
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CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
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OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
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                                                                                                                                  38.38;
63.88;
                                                                                                                                                                    Conservative
                                                mat_peptide
133..861
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Best Local Similarity
Matches 504; Conserv
                                                ; NAME/KEY:
; LOCATION:
US-08-812-025-9
                                  FEATURE:
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/function= "chitinase"
/function= "26 KD preprotein of chitinase G (ChiG)"
/product= "antifungal activity, especially on Trichoderma reesii and Fusarium sporotrichoides as well as Rhizoctonia solani and Botrytis cinerea."
             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petharin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: polyA_signal
LOCATION: 95.310
OCHER INFORMATION: /note= "potential polyadenylation
OTHER INFORMATION: signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
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LOCATION: 862.1002
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3'
                                                                                                                                                                            NAME: KOLE, Lisa
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
TELER: 23855
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: sig_peptide
LOCATION: 298..312
OTHER INFORMATION: /note= "probable signal
OTHER INFORMATION: sequence"
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LOCATION: 349..378
OTHER INFORMATION: /note= "probable signal
OTHER INFORMATION: sequence"
                                                                                                                                                  NAME: Tenser, Arthur REGISTRATION NUMBER: 18,839
                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Hordeum vulgare STRAIN: L.
                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Tenser, Arthur
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466..588
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607..861
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LOCATION: 64..294
OTHER INFORMATION: /nc
OTHER INFORMATION: sec
                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 64..861
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 1..63
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                                                                                                                   FILING DATE:
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LOCATION:
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LOCATION:
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                                                                                          71 cecrococarcorocorocorocorococarcoconarcoconarcocococococo
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                                              42;
    Length 1002;
Score 295.6; DB 1; Length
Pred. No. 1e-50;
0; Mismatches 244; Indels
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/function= "chitinase"
/product= "26 kD preprotein of chitinase G (ChiG)"
/note= "antifungal activity, especially on
Trichoderma reesii and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
                                          Transgenic pathogen-resistant organism
                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/138,873A
FILING DATE: August 24, 1998
ATTORNEY/AGGNT IRFORMATION:
NAME: Tenser, Arthur
REGISTRATION NUMBER: 18,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: polyA_signal
LOCATION: 905..910
OTHER INFORMATION: /note= "potential polyadenylation
OTHER INFORMATION: signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end
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NAME/KEY: sig_peptide
LOCATION: 64..294
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "probable signal peptide sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 862..1002
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFBRENCE/DOCKET NUMBER: A295
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEPAX: (212) 765-2519
TELEPAX: 238655
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                               SEE: Baker & Botts: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kole, Lisa
REGISTRATION NUMBER: 35,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: sig_peptide
LOCATION: 298..312
OTHER INFORMATION: /nc
OTHER INFORMATION: see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                      STATE: New York COUNTRY: U.S.A. ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: 5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: 3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..63
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN: L.
                                                                                                 ADDRESSEE:
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                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 agggcgtgggctcggtcatcacgcggtcggtgtacgcgagcactctgcccaaccgcgaca 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 geaggigicerceargreregegegeacagrirgacegeargererecacegeaacg 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 ACGGCGCCTGCCAGGCCTTCTACACCTACGACGCCTTCGTCGCCGCCGCCGCAGCGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --aaggccacgtccccaccatactatggacggggacccatccaattga 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           431 GCGCACAATGGCCGTGCGCCCCCGGGAAGCGCTACTACGGCCGGGGCCAATCCAGCTCT 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 CCCACAACTACAACTATGGACCTGCCGGCCGGCCATCGGGGTCGATCTGCTGCCGAACC 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         actegetgtgeceggecagaggttetacaegtacgaegeetteategeegeegeeaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 cagggcggtccaactacgatctgccgggagagagcgatcgggaaggacctggtgagcaacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 295.6; DB 4; Length 1002; Pred. No. 1e-50; 0; Mismatches 244; Indels 42;
                                                                                                                                                                                                                           LOCATION: 607...861
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                        /note= "probable signal peptide
                                                                                                                          /note= "probable signal peptide
sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 tecagtggggetactgetteaaggaagagataage--
LOCATION: 349..378
OTHER INFORMATION: /note= "p.
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.3%;
Best Local Similarity 63.8%;
Matches 504; Conservative
                                                                                      NAME/KEY: sig_peptide
LOCATION: 466..588
OTHER INFORMATION: /nc
OTHER INFORMATION: see
                                                                                                                                                                                                     NAME/KEY: sig_peptide
LOCATION: 607..861
                                                                                                                                                                                                                                                                                                                      NAME/KEY: mat_peptide
LOCATION: 133..861
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US-09-138-873A-9
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312 gttccagtggggctactgcttcaaggaagagataagcaaggccacgtccccaccatacta 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 tggacggggaccatccaattgacagggcggtccaactacgatcttgccgggagagcgat 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 TGGTAGAGGACCCATCCAATTGACAAACCGAAATAACTATGAGAAAGCTGGAACTGCAAT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                432 egggaaggacetggtgagcaacceagacetagtgtecaeggaegeggtggtgetetteag 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caacacetteeegggetteggeaceaeeggeagegeegaegaeateaagegegaeetege 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 ggegeagggegtgggeteggteateaegeggteggtgtaegegageaetetgeeeaaeeg 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 516 AACAGCIATATGGTTTTGGATGACACCACAGGACAACAAGCCATCTTCCCACGACGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 GGCACAAGGCATTGGTTCTATTGTAACGAGTGACTTGTTCAACGAGATGCTGAAGAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 egeettetteggeeagaceteecaegagaecaeeggagggaegaggaggeegtgeegaeea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1020;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 239.6; DB 1
Pred. No. 1.3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-19825/P1/CGC 1727
                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UNH-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION DATE: 12-APR-1989
FILING DATE: 12-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEX/AGENT INFORMATION:
MBER: US 07/848,506
6-MAR-1992
                                                                             US 07/768,122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 31.1%;
Best Local Similarity 61.3%;
Matches 424; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (919)541 8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                              27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1020 base pairs
                                FILING DATE: 6-MAR-1'
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 27-SEP-
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-181-271A-7
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        791 AGCGCTACTGTGACATCCTCGGCGTTGGCTACGGCAACAACCTCGATTGCTACAGCCAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
FILING DATE: 13-TAM CLASSITECT:
CLASSITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRICE APPLICATION NUMBER: US 07/678,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/678,378 FILING DATE: 1-ARR-1991 PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/305,566 FILING DATE: 6-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DÀTA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 8-MAR-1988
IOR APPLICATION ...
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                                                                                                                                                                                                                                                                                                                                                                                                              Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                  Sequence 7, Application US/08181271A Patent No. 5614395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shericca C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                                      Ryals, John A.
Alexander, Danny C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moyer, Mary B.
Neuhaus, Jean-Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07 FILING DATE: 21-DEC-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Uknes, Scott J.
Ward, Eric R.
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PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hawtholds STATE: New York
                                                                          755 ggaacttcgc 764
                                                                                                                               851 GACCCTTCGC 860
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APPLICANT: RVALS.
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                               636 TGTAATTACCAACATCATTAACGGTGGAATTGAATGTGGCATAGGACGGAATGACGCAGT 695
612 agtgatcaccaatatcatcaacggcgggtcgagtgcgggaatgggccggaacgccaa
                                                                                             696 GGAAGATCGAATTGGATACTACAGGAGGTATTGTGGTATGTTAAATGTTGTTGCTCCGGGGGA
                                                                    672 egtegacegeateggetaetaeaegegetaetgeggeatgeteggeaeggeeaeggagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OFERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/449,315
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
                                                                                                                                         732 caacctcgactgctacacccagaggaacttcg 763
                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
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APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/181,271
PITTING DATE: 13-JAN-94
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Montoya, Alice
Moyer, Mary B.
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Alexander, Danny C.
Beck, James J.
Duesing, John H.
Grodrich, Leslie B.
Goodman, Robert M.
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Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
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Patent No. 5650505
GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                           Harms, Christian
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MEDIUM TYPE: Floppy
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STATE: New York
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US-08-449-315-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAIICCIIICCIGGIUTIGGAACIACTGGIGAIGAIACIGCCCGIAGGAAAGAAAUTGC 284
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31.1%; Score 239.6; DB 1;
Best Local Similarity 61.3%; Pred. No. 1.3e-39;
Matches 424; Conservative 0; Mismatches 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US C7/368,672
FILING DATE: 20-UN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-MAR-1989
FILING DATE: 12-APR-1983
ATTORNEY/AGENT INFORMATION:
FILING DATE: 6-ARR-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILTING DATE: 20-0CT 1989
PRIOR APPLICATION DATA::
APPLICATION NUMBER: US 07/848,506
FILLING DATE: 6-MAR-1992
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                          PALLING CATTON DATA:
PRIOR PAPLICATION NUMBER: US 07/580,431
FTIING DATE: 7-SEP-1990
                                                                                          APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REPERENCE/DOCKET NUMBER: S-129
REPERENCE/DOCKET NUMBER: S-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8614
IELEFAX: (919)541-8639
INFORMATION FOR SEQ ID NO: 7:
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TYPE: nucleic acid
STRANDEDNESS: single
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MBER: US 07/678,378
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SEQUENCE CHARACTERISTICS:
TRNGTH: 1020 harry
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TELEPHONE: (919)541-8614
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Best Local Similarity 61.3%;
Matches 424; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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EDNESS: single
   APPLICATION NUMBER:
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TOPOLOGY: lin
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                                                                                                                          egicgacegeateggetactacaegegetactgeggeatgeteggeacggecaeeggagg 731
                                                                                                                                                                                                                                                                   696 GGAAGATCGAATTGGATACTACAGGAGGTATTGTGGTATGTTAAATGTTGCTCCGGGGGA 755
      456 TGGACAAGAGCTAGTTAACAACCCTGATTTAGTGGCCACAGATGCTACTATATCATTCAA 515
                                     gacggccatgtggttctggatgacggcgcagggaaacaagccgtcgtgccacaacgtcgc 551
                                                                                                                                                                      612 agtgatcaccaatatcatcaacggcgggctcgagtgcggaatgggccggaacgacgac
                                                                    516 AACAGCTATATGGTTTTGGATGACACCACAGGACAACAAGCCATCTTCCCACGACGTTAT
                                                                                                       cctacgccgctggacgccgacggccgacacaccgctgccggcagggtacccggatacgg
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,803
FILING DATE: 19-MAY-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                     caacetegaetgetacaeecagaggaaetteg 763
                                                                                                                                                                                                                                                                                                                                      756 AAACTTGGACTGTTACAACCAAAGGAACTTCG 787
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16-JUL-1993
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Alexander, Danny C.
Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Mains, Jr., Frederick
Montoya, Alice
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FILING DATE: 13-3AN-94
APPLICATION NUMBER: US 08/093,
FILING DATE: 16-7UL-1993
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Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
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Patent No. 5654114
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 Skyline Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: New York
COUNTRY: USA
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285 IGCCITTICGGICAAACTICICAGGAAACTACIGGIGGATCCCIGAGIGCAG--AACCA 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 caacacetteeegggetteggcaceaeeggeagegeegaegaeateaagegegaeetege 251
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Pred. No. 1.3e-39;
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0; Mismatches 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UNN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
PRIOR DATE: 1-APR-1991
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATE: C-APR-1993
PRIOR APPLICATION DATE: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATE: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATE: US 07/425,504
FILING DATE: 20-OCT 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/768,122 FILING DATE: 27-SEP-1991 APPLICATION DATA: APPLICATION NUMBER: US 07/580,431 FILING DATE: 7-SEP-1990
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FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAY-1992
PRIOR APPLICATION DATA:
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MBER: US 07/580,431
7-SEP-1990
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FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
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24-MAR-1989
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FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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-APR-1991
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PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989

PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAR-1988
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6-MAR-1992
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                              FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                                                                    JMBER: US 08/042,847
6-APR-1993
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              08/181,271
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REFERENCE/DOCKET NUMBER: S-1
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 27-SEP-1991
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REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                            21-DEC-1990
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TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER: US
FILING DATE: 21-DEC-19
PRIOR APPLICATION DATA:
RAPPLICATION NUMBER: US
FILING DATE: 20-OCT 19
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 12-APR-1
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APPLICATION NUMBER: [
FILING DATE: 6-APR-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 TGGACAAGAGCTAGTTAACAACCCTGATTTAGTGGCCACAGATGCTACTATATCATTCAA 515
                                                                                                                                                                                                                                491
                                                        tggacggggacccatccaattgacagggcggtccaactacgatcttgccgggagagcgat 431
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  || || || |-----AGATATIA
                                                                                        396 IGGTAGAGGACCCATCCAATTGACAAACCGAAATAACTATGAGAAAGCTGGAACTGCAAT
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343 TITACAGGAGGTATTGCTTTGTTAGGCAAAATGACCAGAGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08449043
Patent No. 5689044
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Sperison, Christoph
Stinson, Jeffrey R.
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Beck, James J.
Duesing, John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuhaus, Jean-Marc
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US-08-449-043-7
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STATE:
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72 ggcgcagggcgtgggctcggtcatcacgcggtcggtgtacgcgagcactctgcccaaccg 131 132 egacaactegetgtgeeeggeeagaggttetacaegtaegaegeetteategeegeege 191 Query Match
31.1%; Score 239.6; DB 1; Length 1020;
Best Local Similarity 61.3%; Pred. No. 1.3e-39;
Matches 424; Conservative 0; Mismatches 259; Indels 9; S-19825/P1/CGC 1727

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132 cgacaactogctgtgcccggccagaggttctacacgtacgacgccttcatcgccgccgc 191 72 ggogoagggogtgggotcarcacgoggtoggtgtacgcgagcactctgcccaaccg 131 105 GGCACAAGGCAITGGITCTAITGIAACGAGTGACITGITCAACGAGATGCIGAAGAAIAG 164 Gaps caacaccttcccgggcttcggcaccaccggcagcgccgacgtcaagcgcgacctcgc 165 GAACGACGGTAGATGTCCTGCCAATGGCTTCTACACTTATGATGCATTCATAGCTGCTGC 6 Length 1020; Indels S-19825/P1/CGC 1727/DIV10

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                                                                                                                                                                                                                                                                       343 TTTACAGGAGGGTATTGCTTTGTTAGGCAAAATGACCAGAGTGAC-----AGATATTA 395
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252 egeettetteggeeagaeeteeeaegagaeeaeeggaggagggaegagggggegetgeegaeea 311
                                                          285 IGCCTTTTTCGGTCAAACTTCTCACGAAACTACTGGTGGATCCTGAGTGCAG--AACCA
                                                                                                                                                                                                                                                                                                                                                          tggacggggacccatccaattgacagggcggtccaactacgatcttgccgggagagcgat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               732 caacctcgactgctacacccagaggaacttcg 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      756 AAACTIGGACIGITACAACCAAAGGAACTICG 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
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Buesing, John H.

Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
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Williams, Shericca C.
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5.08-455-416-7
Sequence 7, Application US/08455416
Patent No. 5777200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uknes, Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: / J., ST
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APPLICANT: Ryals,
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SULTWARE: Patentin Release #1.0, Version #1.25
CUREMT APPLICATION DATA:
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
NICHARD STATES A STAT
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Pred. No. 1.3e-39;
0; Mismatches 259;
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PRICE AND CATE.

APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-004-1989
PRICE APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRICE APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRICE APPLICATION NUMBER: US 08/045,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/169 6677
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NOMBER: US 07/425,504
FILING DATE: 20-0CT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILLING JOAN PER SPECIAL REPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
RAPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
                                                                                                                                                                                                                                                                                                                                                                US 08/093,301
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,
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REFERENCE/DOCKET NUMBER: S-1
TELECOMMUNICATION INFORMATION:
TET PEDDAME
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Best Local Similarity 61.3%;
Matches 424; Conservative
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ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: single
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APPLICATION NUMBER: C
FILING DATE: 27-SEP-1
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TOPOLOGY: li
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CIBA-GEIGY Corporation
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INFORMATION FOR SEQ ID NO: 7:
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STRANDEDNESS: single
             STREET: / SALL
CITY: Hawthorne
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ADDRESSEE:
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                                                          CITY: Hav
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                   gacggccatgttggttctggatgacggcgcagggaaacaagcgtcgtgccacaagcgtcgc 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             636 TGTAATTACCAACATCATTAACGGTGGAATTGAATGTGGCATAGGACGGAATGACGCAGT 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               egtegacegeateggetactacacgegetactgeggeatgeteggeacggecaceggagg 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                               gttccagtggggctactgcttcaaggaagagtaagcaaggccacgtccccaccatacta 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432 egggaaggacetggtgagcaacccagacetagtgtecacggacgcggtggtgtecttcag 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516 AACAGCTATATGGTTTTGGATGACCACCAGGACAACAAGCCATCTTCCCACGACGTTAT 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agtgatcaccaatatcatcaacggcgggctcgagtgcggaatgggccggaacgacgccaa 671
                                                             343 TITACAGGAGGGTATTGCTTTGGTTAGGCAAATGACCAGAGTGAC-----AGATATTA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tggacggggacccatccaattgacagggcggtccaactacgatcttgccgggagggggt 431
105 GGCACAAGGCATTGGTTCTATTGTAACGAGTGACTTGTTCAACGAGATGCTGAAGAATAG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CALLIANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stanson, Jeffrey R.
APPLICANT: Ward, Eric R.
APPLICANT: Wald, Eric R.
APPLICANT
                                                                                                                                                                                                    caacacetteecegggetteggeaceaceggeagegeegaegaeateaagegegaeetege
                                                                                                                                                                                                                                             732 caacctcgactgctacacccagaggaacttcg 763
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Alexander, Danny C.
Beck, James J.
Duesing, John H.
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APPLICANT:
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APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-19825/P1/CGC 1727
                                                                                                                                                                                                                                                                                                                                        CATACLA REFLACATION NUMBER: US/08/455,244
PILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: 08/093,301
FILING DATE: 16-UIL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-VUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-APP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,566
FILING DATE: 6-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
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FILING DATE: 20-0CT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATI
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APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
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24-MAR-1989
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APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 35,129
REFERENCE/DOCKET NUMBER: 5-
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/165,667 FILING DATE: 8-PAR-1988 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/042,847 FILING DATE: 6-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/425,504 FILING DATE: 20-0CT 1989 APPLICATION DATA: APPLICATION NUMBER: US 07/848,506 FILING DATE: 6-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/305,566 FILING DATE: 6-FEB-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/632,441 FILING DATE: 21-DEC-1990 PRIOR APPLICATION DATA:
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20-JUN-1989
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APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-UUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
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1-APR-1991
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                                                                                                                                                                                                      CIBA-GEIGY Corporation
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APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08/181,271
                                           Uknes, Scott J. Ward, Eric R. Williams, Shericca C.
Sperison, Christoph
Stinson, Jeffrey R.
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REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                                            : 7 Skyline Drive
Hawthorne
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APPLICATION NUMBER: US
FILING DATE: 27-SEP-19
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US
FILING DATE: 7-SEP-199
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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APPLICATION NUMBER: U
FILING DATE: 1-APR-15
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy
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FILING DATE: 12-AP
                                                                                                                                                                                                                                                                         New York
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                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 TGCCTTTTTCGGTCAAACTTCTCACGAAACTACTGGTGGATCCCTGAGTGCAG--AACCA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                       311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 gttecagtggggetactgetteaaggaagagataageaaggeeaegteeeeaeeataeta 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372 tggacggggacccatccaattgacagggcggtccaactacgatcttgccgggagagcgat 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 TGGTAGAGGACCCATCCAATTGACAAACCGAAATAACTATGAGAAAGCTGGAACTGCAAT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 egggaaggacctggtgagcaacccagacctagtgtccacggacgcggtggtgtccttcag 491
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                                                                                                                                                           ggegeagggegtgggeteggteateaegeggteggtgtaegegageaetetgeeeaaeeg 131
                                                                                                                                                                                                                                                    105 GGCACAAGGCATTGGTTCTATTGTAACGAGTGACTTGTTCAACGAGATGCTGAAGAATAG 164
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 AACAGCTATATGGTTTTTGGATGACACCACAGGACAACAAGCCATCTTCCCACGACGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  552 cctacgccgctggacgccgacggccgccgccgccgctgccggcagggtacccggatacgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             612 agigatcaccaatatcatcaacggcgggctcgagigcggaaigggccggaacgacgaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    636 TGTAATTACCAACATCATTAACGGTGGAATTGAATGTGGCATAGGACGGAATGACGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               672 cgtcgaccgcatcggctactacacgcgctactgcggcatgctcggcacggccaccggagg
                                                                                                                                                                                                                                                                                                                                                                                                                                       252 egecttetteggeeagaceteceaegagaceaegagaggaggaegagggegetgeegaeea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 ITTACAGGAGGGTATTGCTTTGTTAGGCAAAATGACCAGAGTGAC-----AGATATTA
                                                                                                                                                                                                                                                                                                                                                 caacaccttcccgggcttcggcaccaccggcagcggcgacgacatcaagcgcgacctcgc
                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                   Length 1020;
                                                                                                                Indels
                                                                   Score 239.6; DB 1;
Pred. No. 1.3e-39;
0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               732 caacctcgactgctacacccagaggaacttcg 763
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Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alexander, Danny C.
Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08454876
Patent No. 5804693
GENERAL INFORMATION:
APPLICANT: RYALS, John A.
APPLICANT: Beck, James J.
APPLICANT: Beck, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
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Harms, Christian
                                                                31.1%;
ilarity 61.3%;
Conservative
                                                                   Query Match
Best Local Similarity
Matches 424; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
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APPLICANT:
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US-08-454-876-7
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       US-08-455-244-7
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APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUFFWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,364
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
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20-OCT 1989
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FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/580,431 FILING DATE: 7-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/632,441 FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                         CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
             Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,:
                                                                                                                                                 Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                             Moyer, Mary B.
Neuhaus, Jean-Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-1989
John H.
                                                                                                                                                                                                           Uknes, Scott J.
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CIBA-GEIGY Co
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 21-DEC-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 20-OCT 19
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                           Ward, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 6-APR-19
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                       10532
                                                                       APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                               Score 239.6; DB 1
Pred. No. 1.3e-39;
0; Mismatches 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08457364
Patent No. 5847258
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Beck, James J.
                                                                                                                                                                                                                                 tch 31.1%;
al Similarity 61.3%;
424; Conservative
 TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                         LENGTH: 1020 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 424; Conserva
                                                                                                                                                       ; MOLECULE TYPE: cDNA
US-08-454-876-7
                                                                                                                                         linear
                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 gttccagtggggctactgcttcaaggaagagataagcaaggccacgtccccaccatacta 371
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31.1%; Score 239.6; DB 2; Length 1020;
Best Local Similarity 61.3%; Pred. No. 1.3e-39;
Matches 424; Conservative 0; Mismatches 259; Indels 9;
FILING DATE: 24-MAR-1989

PRIOR APPLICATION DATA:

#PRIOR DATE: 10.08 08/045,957

FILING DATE: 12-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Elmer, James Scott

REGISTRATION NUMBER: 5-19825/P1/CGC 1727

TELEPHONE: (919)541-8614

TELEPHONE: (919)541-8619

TELEPHONE: (919)541-8619

TELEPHONE: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1020 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-457-364-7
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Search completed: May 3, 2002, 16:26:33 Job time: 7267 sec

HV_CED001 WHE0667_G HV_CEa001 HVSMEa001

HVSMEa000

WHE0505_G HV_CED000 WWS05.GBR HVSME£001

HVSMEa000 WHE0562_G Zm10_06h0

Talr1156A HV_CEa000

HVSME1000

19 HV_CEa001 C72797 Rice

707097F10 HVSMEh010

DB DB

Minimum Maximum

Searched:

Sequence:

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Database

1264374321 110987654321

No.

Sc02_08b0

HVSMED001 HVSMED009 HVSME1000 945005H06

Zm10_02h0 945020E07 Zm10 03a0

HVSMEK000

nucleic

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Run on:

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Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 906)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo Wood, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF065825 906 bp mRNA EST 09-MAR-2001

HV_CEb0014B14f Hordeum vulgare seedling green leaf EST library
HVCDMA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone

HV_CEb0014B14f, mRNA sequence.

BF065825. GI:13265390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Development of a genetically and physically anchored BST resource for barley genomics pubblished (2000) On Oct 17, 2000 this sequence version replaced gi:10842464.
                                                                   BES8767 BES87679 W
                                                                                                                                                                                       BF259671 FBF624096 FBE493038 V
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BE602548 F
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BG837580 9
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BG414551 F
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Hordeum vulgare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 749.
Location/Qualifiers
1. .906
                                                                                                                                                             BE215793
BE420363
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Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
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355.2
305.2
236.6
250.2
495.4
442.4
434.2
432.4
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Contact: Wing RA
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/clone_lib="Fordeum vulgare seedlit
library WrCDNa0005 (Erysiphe infect
/tissue_type="seedling green leaf"
/lab_host="SolR"
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Pred. No. 2.3e-110;
0; Mismatches 59; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University Genomics Institute Clemson University
100 Jordan Hall, Clemson, SC 29634, US Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Institute
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/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
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llarity 91.8%;
Conservative 0
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Matches 659; Conserv
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HV_CED0013H08f Hordeum vulgare seedling green leaf EST lbrary HVCDD001056 (Erysiphe infected & control) Hordeum vulgare cDNA clone HV_CED0013H08f, mRNA sequence.
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Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                      catcacgcggtcggtgtacgcgagcactctgcccaaccgcgacaactcgctgtgcccggc 152
                                                                                                                                                                                                                                                                                                                                                                      caccacoggoagogacgacatcaagogogacctcgccgccttcttcggccagacctc 272
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                                                                                                                                                                                                                                           cagagggttctacacgtacgacgccttcatcgccgccgccaacacttcccgggcttcgg 212
                                                                                                                                                                                 362 GACAGGGCAGTCCAACTACGATCTCGCCGGGAGGGCGATCGGGGAAGGACCTTGTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         632 acggoggctcgagtgcggaatgggccggaacgacgccaacgtcgaccgcatcggctact
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                                                                                                           5;
                                                                      Length 937;
                                                                                                           Indels
                                                                      10;
                                                                      Score 597.6; DB 10,
Pred. No. 2.3e-105;
0; Mismatches 74;
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 264
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89.7%;
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 280
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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HV_CEb0024H02f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
BE559387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders"
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1 (bases 1 to 937)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu., Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Development of a genetically and physically anchored EST resource for barley genomics Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
CAAGGAGGAGATAAACAAGGCCACGTCCTACTATGGACGGGACCCATTCAATT 452
                                                                         453 occagacetagtgtccacggacgcggtggtgtccttcaggacggccatgtggttctggat 512
                                                                                                                                                                                                        513 gacggegeagggaaacaageegtegtgeeacaaaegtegeeetaegeegetggaegeegae 572
                                                                                                                                                                                                                           ggccgccgacaccgctgccggcagggtacccggatacggagtgatcaccaatatcatcaa 632
                                                                                                                                                                                                                                                                                                                   633 GGCTGCCGATACAGCTGCAGGTCGGGTGCCTGGATACGGCGTAATCACCAATATCATCAA 692
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                                                      452
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/tissue_type="seedling green leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                              cacgegetaetgeggeatgeteggeaeggedaecggaggeaacetegaetgetaeaee 750
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                                                          gacagggcggtccaactacgatcttgccgggagagcgatcggggaaggacctggtgagcaa
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Fax: 864 656 4293
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/db_xref="taxon:4513"
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Seg primer: AarraAcCCCTCACTAAAGGG
High quality sequence stop: 586.
Location/Qualifiers
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Wood,T.
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SOURCE

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BF065067 829 bp mRNA EST 09-MAR-2001
HV_CEb00022N01f Hordeum vulgare seedling green leaf EST library
HVCED0A0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
BY CEb0022N01f, mRNA sequence.
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1 (bases 1 to 829)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, X., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Slmmons, J., Choi, D.W., Main, D. and Wood, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                   702 GAACCGACCCCAACGTCGAATGGATTGGTGTACTTAAAGCCCCTTATGGAGGATTGCTGG 761
                                  gtgteetteaggaeggeeatgtggttetggatgaeggegeagggaaacaageegtegtge
                                                                 cacaacqtcqccctacqccqctggacqccqacqqccgccgacaccgctgccggcagggta
                                                                                                                                                                        ggaacgacgacaacgtcgaccgcatcgg---ctactacacgcgctactgcggcatgctcg
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/clone_lib="Hordeum vulgare
library HVcDNA0005 (Erysiphe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Hordeum vulgare"
/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
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Seq primer: AATTAACCCTAAAGGG
High quality sequence stop: 589.
Location/Qualifiers
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90.98;
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Unpublished (2000)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                         Triticeae: Hordeum.

1 (bases 1 to 923)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,X., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and Wood,T.
                                                                                                                                                                                          Development of a genetically and physically anchored EST resource
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/clone_1hb-"Hordeum vulgare seedling green leaf EST
/Library HVCDNA0005 (Erysiphe infected & control)"
/tissue_type-"seedling green leaf"
/lab_host-"SOLR"
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                                                                                                                                                                                                                                          Unpublished (2000)
On Oct 17, 2000 this sequence version replaced gi:10842333.
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Pred. No. 9.5e-104;
0; Mismatches 93;
                                                                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
Clemson University
100 Uordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/organism~"Hordeum vulgare"
/cultivar="C116151 (Mla6)"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 640.
Location/Qualifiers
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||Iarity | 87.2%;
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Contact: Wing RA
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/clone_lib="Hordeum vulgare seedling green leaf EST library HVcDNA0005 (Erysiphe infected & control)" /tissue_type="seedling green leaf" /lab_host="SolR" /note="Vector: lambdaZAP; Site_l: EcoRl; Site_2: Xhol; Fox more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 247 c 270 g 167 t Score 569.6; DB 11; Length 829; Pred. No. 5.4e-100;

COMMENT Clemson University Clemson University Clemson University Clemson University Clemson University Clemson University Clemson Set 4293 Email: wingGedlemson.edu Seq primer: AATTAACCTCACTAAAGGG High quality sequence stop: 860. FEATURES Location/Cualifiers Location/Cualifiers Location/Cualifiers Location/Cualifiers Location/Cualifiers Colone="HV-CED0014L16f" / Colone="HV-CED0014L16f" / Colone="HV-CED0014L16f" / Colone="HV-CED0014L16f" / Lissue_type="seedling green leaf BST / Clone="HV-CED0014L16f" / Lissue_type="seedling green leaf" / L	Ouery Match Best Local Similarity 90.0%; Pred. No. 8.66-100; Matches 667; Conservative 0; Mismatches 64; Indels 10; Gaps 5; Matches 667; Conservative 0; Mismatches 64; Indels 10; Gaps 5; Qy 1 atggcgaggttgctgccgcgtgtgcgccgcgcgctcctgctgcgcgggggg	Oy 301 gctgccgaccagttccagtggggctactgcttcaaggaagataagcaaggccacgtcc 360 391 GccGcGaCCATCCATGGGCTACTCATGAGGAAGAGAAGCAGGCCT 450 bb 391 GccGCGACCATTCCAATGGGCTACTCATCAGGAGAGAAGCAGGCCAGGTCT 450 Cy 361 ccaccatactatggaccgggaccatcgacttgacagggggggg
Qy 84 gggctcggtcatcacgcggtcggtgtacgcgagcactctgcccaacgcggacaac-t 139 2; Qy 84 gggctcggtcatcacgcggtcggtgtacgcgagcactctgcccaacacct 139 11	OY 440 acctggtgagcaacccagacctagtgtccacggacggtggtgctcttcaggacggcca 499 385 ACTTGTGAGCAACCCGGATCTGTTCACGGACGCGTGGTCCTTCAGGACGCGA 326 QY 500 tgtggttctggatgacggcagcagcagcagcgcgcgtgtgccacaacctcagcc 559 325 TGTGGTTCTGGATGACGACCCGACCCGAGCCCAAACGCCGCCCTACGCC 266 QY 560 gctggacgcggcgacacagcgcgcagcagcagcagcagcagca	RESULT 6 BF066058 BF066058 BF066058 HV_CED0014L16f Hordeum vulgare seedling green leaf EST library HVCDN0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone HV_CED0014L16f, mRNA sequence. HV_CED0014L16f, mRNA sequence. BF066058 SET 09-MAR-2000 BF066058 SET 08-MAR-2000 BF066058 SET 08-MAR-200 BF066058 BF066058 SET 08-MAR-200 BF066058 BF06605

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wing, R., Closs, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                                      BF264498 842 bp mRNA EST 09-MAR-2001 HV-CDE0009J09f Hordeum vulgare seedling green leaf EST library HYCDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone HV_CE00009J09f, mRNA sequence.
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255 c 255 q 143 t
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691 TCAGGGCTCCGGGGTATCCCCAAATATCATCAACGGGGGGCCTCAAGTGCGGGATGGGCC 750
                                   -cat 710
                                                                    751 cegaaceacecccaacercaarcecriseerractaacaceccracresegeaarre 810
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Onpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11195492.
Contact: Wing RA
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                                   658 eggaacgaeg-ceaaegtegaeegeateggetaetaeaegegetaetgegg-
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Tel: 864 656 7288
Fax: 864 656 4293
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/db_xref="taxon:4513"
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Seq primer: AATTAACCCTCACTAAAGGG
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Location/Qualifiers
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BF264498.2 GI:13261550
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                                                                                                                                              811 GCTCGGCACGGCCACCGGGGG 831
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91.4%;
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Eukaryota; "Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (bases 1 to 669)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Y., Anderson, H., Dale, J., Henry, D., Kernodde, S., Palmer, M., Rambo, T., Saki, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
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HV_CED0006009f Hordeum vulgare seedling green leaf EST library
HVCDRA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CED0006009f, mRNA sequence.
BE215473. GI:13264441
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                                                                                                gecacytececatectatygacygygacecatecaattyacagygegytecaaetae 411
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                                                                                                                                                                                                                                                                                                                                            303 GATCTCGCCGGGAGGCGATCGGGAAGGACCTTGTGAGCAACCCGGATCTGGTGTCCACT 362
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472 gacgcggtggtgtccttcaggacggccatgtggttctggatgacggcgcagggaaacaag
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On Jul 3, 2000 this sequence version replaced gi:8903085.
Contact: Wing RA
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Clemson University
100 Jordan Hall, Clemson, SC 29634, UE
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/cultivar="C116151 (Mla6)"
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Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 644.
Location/Qualifiers
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Fax: 864 656 4293
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ilarity 91.9%;
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                                     Triticeae; Hordeum. (bases 1 to 695)
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HV_CEb0003N19f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
BE214577
                                                                              For
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                                                                                       more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 223 c 214 g 107 t l others
        /clone="HV_CEB00066099f"
/clone_lib="Hordeum vulgare seedling green leaf EST library HVDNA0005 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/lab_host="%OLR"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                                                                                                                                                                                                                                                                                                                                                                                                   240
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                                                                                                                                                                                                                                       Length 669;
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                                                                                                                                                                                  Score 545.4; DB 10;
Pred. No. 2.3e-95;
0; Mismatches 42;
/db_xref="taxon:4513"
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae
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227 c 218 g 116 t 1 others
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                                                                                                                                                                                             Development of a genetically and physically anchored EST for barley genomics for barley genomics on Jul 3, 2000) on Jul 3, 2000 this sequence version replaced gi:8902189. Contact: Wing RA
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Pred. No. 4.7e-94; 
0; Mismatches 50; Indels 0;
                                                                                                                                                                                                                                                                                                                                                          Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel 100 464 656 4293
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University Genomics Institute
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Qy 262 ggccagacctccca Db 62 ggccagacctcccc Qy 322 ggctactgcttcaa Qy 322 ggctactgctrcaa Db 122 gGcTactgcTrcAa Qy 382 cccatccattgac Db 182 cccatccattgac Qy 442 ctggtgagacacc Qy 442 ctggtgagacacc Qy 442 ctggtgagcaccc Db 242 cTtGtGAGCAACCC	Oy 502 tggttctggatgac	682 4 6 4 6 4 6 6 8 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT 11 BF628657 LOCUS DEFINITION HVSMED0006PO ACCESSION BF628657 VERSION BF628657 VERSION BF628657 KEYWORDS SOURCE BAILEY	ORGANISM HOrdeum vilg Eukaryota; v Spermatophyr; Triticae; Triticae; Triticae; Triticae; AUTHORS Wing,R., Clo Y., Anderso Y., Anderso Y., Anderso Y., Saski,C Wood,T. TITLE Development for barley g COMMENT On Dec 19, 22	urce
	RESULT 10 BE214283 LOCUS BE214283 LOCUS DEFINITION HY_CEDB0003A01f Hordeum vulgare seedling green leaf EST library HYCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone HY_CEB0003A01f, mRNA sequence. BE214283 VERSION BE214283.1 GI:8901895 KEYWORDS		ы	reducks 10.725 Corganism="Hordeum vulgare" /cultivar="reliafis1" (Mla6)" /db_xref="taxon:4513" /db_xref="taxon:4513" /clone="Hy_CEBO003A01f" /clone="Hy_CEBO003A01f" /clone="Hy_CEBO003A01f" /clone="Hy_CEBO003A01f" /clone="Hy_CEBO003A01f" /clone="Hy_CEBO003A01f" /lab="Hordeum vulgare seedling green leaf EST library HyCDNA0006 Erysiphe infected & control)" /tissue_type="seedling green leaf" /lab_host="SOLR" /note="Vector: lambdaZAP; Site_1: EcoRl; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/parley/ To	DASE COUNT 165 a 226 c 211 g 123 t ORDERSON.edu/orders

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Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
rta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
e; Hordeum.
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HV_CED0009C12f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CED0009C12f, mRNA sequence.
BE216024.1 GI:8903636
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                                                                                                                                                                             Length 713;
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                                                                                                                                                                 acggcgggctcgagtgcggaatgggccggaacga 665
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
'Triticeae; Hordeum.
1 (bases 1 to 583)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu.Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo Wood,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
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Pred. No. 7e-86;
0; Mismatches 26;
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
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/organism="Hordeum vulgare"
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/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCCTGACTAAAGGG
High quality sequence stop: 581.
Location/Qualifiers
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95.28;
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Unpublished (2000)
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Best Local Similarity 95.2
Matches 511; Conservative
                                                                                                                                                                                                                                                                                        Contact: Wing RA
Hordeum vulgare
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us-09-534-229c-6.rst

	Qy 241 egegacetegeegettettege 		Db 412 TCACCCTACTATGGACGGGACC QY 421 gggagagcgatcgggaaggacct	532	Db 592 CAACACTTAG-CCTACTCCGCTC QY 601 cccggatacggagtgatcaccaa	Qy 66C gaacgacyccaacgtcgacc 	RESULT 14 BF266125 LOCUS LOCUS LOCUS BF266125 S76 bp DEFINITION HV.CEa0014D24f Horder HV.CEa0014D24f, mRNA ACCESSION BF266125 VERSION REYNORDS SOURCE SOURCE ORGANISM HORDER BATLEY ORGANISM HORDER BYAGTON KANDON SOURCE BYAGTON CHARLEY SOURCE	RS	TITLE Development of a gene for barley genomics JOURNAL Unpublished (2000) COMMENT ON NOV 17, 2000 this CONTACT: Wing RA Clemson University Ge Clemson University Ge 100 Tochan Hall Clem	Tel: 864 656 7288 Frax: 864 656 4293 Email: rwingeclemson. Seq primer: AATTAACCO. High quality sequence
GGGAGAGCGATCGGGAAGGACCTTGTGAGCAACCCGGATCTGGTGTCTCCACGGACGCGGT	481 gigtecetteaggageaggeagtggftetggatgaeggaggaggaggagagcgteg 537 			; Triticeae; Hordeum. ; Micker 1 (bases 1 to 923) ; Heinhofs,A., Wise,R., Begum,D., Frisch,D., Yu for Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu ,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo ,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and	AL	Clemson University 100 Jordan Hall, Clemson, SC Tel: 864 656 4293 Email: rwingGelemson.edu Seg primer: AATTAAACCCTACACAA High quality sequence stop: 1.9237	/organism="Hordeum vulgare" /cultivar="Cinisis" (Mia6)" /db_xref="taxon:4513" /clone="HV_CEb0024F08f" /clone="HV_CEb0024F08f" /clone="HV_CEb0024F08f" /clone="HV_CEb0024F08f" /tissue_type="seedling green leaf" /tissue_type="seedling" /tissue_type="seedling green leaf" /tissue_type="seedling green	.ch 11 Similar: 640; Cons	1 atggogaggtttgctgccctcgccgtgtgcgccgcgctcctgctcgccgtggcgcg 60	
qa 8	d D	RESULT 13 BE559371 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURN COMMENT	FEATURES	BASE COUNT	ORIGI Que Bes Mat	0y 0y 0y	Qy Dp

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HV_CEa0013NO9f Hordeum vulgare seedling green leaf EST library
HVCDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae
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                                                                                      /tissuê_type="seedling green
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                                            ,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and Wood,T.
Development of a genetically and physically anchored EST resource
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Ramb,
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. an
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On Nov 17, 2000 this sequence version replaced gi:11196972.
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Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
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Oryza sativ

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X56787 O.sativa L.

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1 (bases 1 to 1186)
Nishizawa,Y., Kishimoto,N., Saito,A. and Hibi,T. Sequence variation, differential expression and chromosomal location of rice chitinase genes

Mol. Gen. Genet. 241 (1-2), 1-10 (1993)
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AB015655 Cucurbita AB048531 Psophocar E13289 cDNA encodi

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E13290 123881 Embryophyta; Tracheophyta;

SUMMARIES

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PLN

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DB seq DB seq

Minimum Maximum Database

Total number

Searched:

Perfect score:

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Sequence:

Scoring table:

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GAGACCACCGGCGGGTGGCCGACCGCGCCCCGACGGCCCTTCTCCTGGGGGCTACTGCTTC 528
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IGYDLLSNPDLYATDATVSFKTALWFWMTPQGNKPSSHDYITGRWAPSPADAAAGRAP
GYGYITNIYNGGLECGHGPDDRYANRIGFYQRYCGAFGIGTGGNLDCYNQRPFNSGSS
                                                                                                                                                                                                                                        PNCLCCSRWGWCGTTSDFCGDGCQSQCSGCGPTPTPTPPSPSDGVGSIVPRDLEERLL
LHRNDGACPARGFYTYEAFLAAAAAFPAFGGTGNTETRKREVAAFLGQTSHETTGGWP
                                                                                                                                                                                                                              /translation="MSTPRAAASLAKKAALVALAYLAAALATAARAEQCGAQAGGARC
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Direct Submission
Submitted (13-NOV-1990) Y. Nishizawa, NATIONAL INSTITUTE OF
AGROBIOLOGICAL RESOURCES, TSUKUBA SCIENCE CITY, KANNONDAI, IBARAKI
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                                                                                                                                                                                                                  /db_xref="SPTREMBL:043294"
                                                                                                                                                                                                                                                                                                                                                                                                        161
                                                                                                                                                                                          /protein_id="CAA40107.1"
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106. .228
                                                                                                                                 /product="chitinase"
10. 1032
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                                                                                                                                                                                  /product="chitinase"
                                            Location/Qualifiers
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                                                                                                              /clone="RCC2"
10. .105
                                                                                                                                                                        /codon_start=
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1057. .1062
1150. .1155
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoph;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases I to 1779)
Leah,R.; Skriver,K.; Knudsen,S., Ruud-Hansen,J., Raikhel,N.V.
                                                                                                                                                                                                                                                                                                               999cagaacgacaaggtggcggatcggatcgggttctacaagcgctattgtgacattttc 900
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aagcaggagcagggctcgccgccgagctactgcgaccagagcgccgactggccgtgcgca
                     cccggcaagcagtactatggccgcggccccatccagctcacccacaactacaactacgga
                                                                                            coggocgogogaatcggggtggacctgctgaacaatccggacctggtggccacggac
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Hordeum vulgare chitinase (CH133) gene,
L34211
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682. .1680
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/gene="CHI33"
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PLN complete cds.
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Pred. No. 1.5e-68;
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1. .1291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=experimental
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                                                                                                                                                                                             Oryza sativa chitinase mRNA,
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1291
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75.4%;
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43. .111
43. .1044
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                        /Traislation="MRQPSVVAIVAIVAIVABALAMANVYRAQOCGSQAGGATCPNCLC
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INGGLECGRGADSRVADRIGFYQRYCNILGVGYGGNLDCYNQRPFVBGLLIQRVTE"
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                                                                                                                                                                                                    27;
                                                                                                                                                                         DB 8; Length 1779;
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                                                                                                                                                                        Score 569.6; DB 8;
Pred. No. 7.4e-69;
0; Mismatches 199;
                                                                                                                 379 t
                                                                                                                                                                                                                                gogacggccgtcctggccgtcgtcctggcggcg---
/protein_id="AAA56787.1"
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                                                                                                                475 g
                                                                                                                                                                      Query Match 58.6%;
Best Local Similarity 76.7%;
Matches 746; Conservative
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GPSKWYCKRELAAAASVCVASAEWPCAADKKYFGROLDGSYNWYDGAGBATGED
LLNNPELYASDPVVERTALMFWMTPOSPKSCHDVITGOWTPSSODIAAGRYPGYGY
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/evidence=experimental
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Organ sativa

Divaryopta: Viridiplantae; Streptophyta; Embryophyta; Tra

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaces

Ehrhartoideae; Oryzeae; Oryza.

Loases 1 to 1291)

Yun,C.-H., Kim,J.-K. and Park,Y.-H.

Isolation and Characterization of A Rice Chitinase CDNA

Unpublished (1994)
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Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
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Pooldeae; Poeae; Poa.

1 (bases 1 to 1173)

Du,M. and Ha,S.B.

Direct Submission

Submitted (22-APR-1997) Plant Biology, U.C. Berkeley,

94706, USA
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                                                                                                                                           /organism="Poa pratensis"
/strain="Glade"
/db_xref="taxon:4545"
194. .346
                                                                                                         Location/Qualifiers
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/gene="chi3"
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/gene="Chi3"
/note="chitinase"
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/pseudo
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Local Similarity 76.3%;
Les 714; Conservative (
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Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta; Liliopsida, Poales, Poaceae, Pooideae, Triticeae,
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Yeh,S., Moffatt,B., Griffith,M., Xiong,F., Yang,D.S.C.,
Wiseman,S.B., Sarhan,F., Danyluk,J., Xue,Y.Q., Hew,C.L.,
Doherty-Kirby,A. and Lajoie,G.
Chitinase genes responsive to cold encode antifreeze proteins in
winter cereals
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Secale cereale 31.7 kDa class I endochitinase-antifreeze protein
precursor, mRNA, complete cds.
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                                                    CCCACGCCGGTGACCCCGGACTCCCTCCGGCGGCGCGTGTCCTCCATCGTATCTCAG
                                                                                                            gacctcttcgagcggttcctgctccatcgcaacgacgcagcgtgcctggcccgcggggttc
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GTTSDYCGFGCQSQCNGCSGFTPVTPPSGGGGVSSTYSQSLFEQMLLHRNDAACLAK
GFTYNAFIAAANSFAGFGTTGSTPVYFRFRPAFLAQTSHFTTGGWFPAFDGPYSNGY
CFKQEGGATTAAANSFAWCAPGKFYFRFRPTIGTSTYNTYGFAGQATQTDLINNFDL
VATDPFYSFKTALMFWMTAQSFFSSHAVITGGWSFSSADQAAGFVPGGYTNIING
GLEGGKGQDNRVADRIGFYKRYCDLLGVSYGNNLDCYSQRFFGS"
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                                                                                                                                                                                                                                                             1055 GCCGACAGGATCGGGTTCTACAAGCGCTACTGCGACCTCCGGCGTCAGGCGGGGAC 1114
                                                                                                                                                                                                              gcggatcggatcgggttctacaagcgctattgtgacattttcggcatcggctacgggaat 918
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  acggggctgtggactccgacggccagggatagcgcaggccggacgggtacccgggtatggt 798
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0; Mismatches 203;
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/codon_start=1
/product="chitinase"
/protein_id="AAR04454_1"
/db_xref="GI:6164588"
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/db_xref="taxon:4545"
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GSTSBYCGGOGQSQCBNCGGTPVPVPPTGGGVSSISQSCHFPDQMLAHNDAACLAKG
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FYNGAFIAAANSFSRATGGTDVBKREVAAFLAGTSHFTTGGWPTAPDGFYSWGYC
FNQERGAPSDYCSPSSQWPCAPGKKYFGRGPIGISINYNYGPAGRAIGTDLLNNPDLV
ATDATVSFRALWFWMTPQSPKRSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGG
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389 C
204 L
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                                                                    Submitted (20-JUN-2000) Biology, University of Waterloo, University Ave West, Waterloo, ON N2L 3G1, Canada Location/Qualifiers
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                                             and Hew, C.L
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Pred. No. 3.2e-65;
0; Mismatches 211;
                            2 (bases 1 to 1192)
Yeh,S., Moffatt,B., Griffith,M., Xiong,F.
Direct Submission
 Plant Physiol. 124 (3), 1251-1264 (2000)
                                                                                                                              /organism="Secale cereale"
                                                                                                                                                                                                                                                                              /protein_id="AAG53609.1"
/db_xref="GI:12407647"
                                                                                                                                               /variety="Musketeer"
/db_xref="taxon:4550"
                                                                                                                                                                                                                                                                       protein precursor"
                                                                                                                                                                              /chromosome="1"
                                                                                                                                                                                                                                       /codon_start=1
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75.0%;
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RNDGACRAAGFYTYEAFLRRAAFPAFGGTGDJTSTRKREVAAFLGQTSHETTGGWPTAP
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Muratha.C.S., Mew.T. and Muthukrishnan,S.
Induction of Chitinases and beta-glucanases in Rhizoctonia solani
infected rice plants: Isolation of an infection-related chitinase
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa IR58 chitinase mRNA, complete
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/db_xref="taxon:4530"
/clone="clone RC-7"
/tissue_type="leaf"
/clone_lib="lambda GTII"
/dev_stage="mature"
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/organism="Oryza sativa"
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/EC_number="3.2.1.14"
/function="hydrolyzes
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Muthukrishnan,S.
Direct Submission
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/translation="MRGVVVVVMLAAAPAVSAHAEQCGSQAGGATCPNCLCCSKEGFC
GSTSDYCGNGCOSQCNGCSGGGTPVPVPTPTGGGVSSIISQSLFDQMLLHRNDAACQA
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YCFNOREGAASDYCSPNSQWPCAPGKKYFGRGF1GSYNYNYGPAGRAIGTDLINNPD
LVATDATVSFKTALWFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVUTININ
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                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae, Triticeae, Triticum.
884 GACGACCGCGTGGCAAACCGGATCGGCTTCTACCAGGCCTACTGCGGGGGGGTTCGGCATC 943
                                                                         1001
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Submitted (09-NOV-1993) Y. Liao, Inst. fuer Biologie I, RWTH
Worringer Weg, 52056 Aachen, FRG
2 (bases 1 to 1985)
                                30;
                                                                                                                                                           T.aestivum (Chinese spring) chi gene for endochitinase. X76041
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/cultivar="Chinese spring"
/db_xref="taxon:4565"
/clone_lib="lambda gem-12 genomic"
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Pred. No. 1.7e-64;
0; Mismatches 211;
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/protein_id="CAA53626.1"
/db_xref="G1:416029"
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529. 52
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/gene="CHI"
71. .75
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250. .254
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390. 254
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/gene="CHI"
633. .1595
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/gene="CHI"
693. .1592
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/gene="CHI"
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Best Local Similarity 74.5
Matches 704; Conservative
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                     GIGGIGGICCAIGCIGGCCGCGCGCCIIICGCCGIGICIGCGCACGCCGAGCAGIGCGGC
                                           tegeaageeggeggegaagtgegeegactgeetgetgeageeagttegggttetge
                                                       ggcaccacctccgactactgcggcccccgctgccagagccagtgcactggctgcggtggc
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gtoctggccgtcgtcctggcggcggcggcggtcacgccggccacggccgagcagtgcggc
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HVU02287 1684 bp DNA PLN 30-MAY-1994 GOZGEUM VULGATE CULLIVAR NK1558 Chitinase gene, complete cds. U02287

GI:495304

U02287.1 barley.

DEFINITION ACCESSION VERSION KEYWORDS

SOURCE

RESULT HVU02287 LOCUS

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Abstate="01:495305"
/translation="MARFVLEWVAMAATMAVAEOCGSDAGGATCPNCLCCSRFGWCG
STPYCGDGCQSQCSGCGGGSTPVTPTPSGGGGVSSIVSRALFDRMLLHRNDGACQAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FYTYDAFVAAASAFRGFGTTGGTDTRKREVAAFLAQTSHETTGGWATAPDGAFAWGYC
FKQERGATSNYCTPSAQWPCAPGKSYYGRGPIQLSHNYNYGPAGRAIGVDLRNPDLV
ATDPTVSFKTAMWFWMTAQAPKPSSHAVITGQWSPSGTDRAAGRVPGFGVITNIVNGG
Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.

1 (bases I to 1684)
Ignatius, S.N.J., Huang, J. and Muthukrishnan of Isolation and Articles.
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                                                                                                                                                                                          Kansas State University,
66560, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1684;
                                                                                     Ignatius, S.M.J., Huang, J. and Muthukrishnan, S. Isolation and characterization of a barley chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IECGHGQDSRVADRIGFYKRYCDILGVGYGNNLDCYSQRPFA"
600. .656
657. .1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                   Direct Submission
Submitted (29-SEP-1993) Muthukrishnan S., I
Biochemistry, Willard Hall, Manhattan, KS
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206;
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/function="hydrolyzes
/product="chitinase"
514 c 471 g
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/function="hydrolyzes
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74.9%;
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Muthukrishnan, S.
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600. .1556
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Obtoura, T. Yamagami, T. and Ishiguro, M. Direct Submission

Direct Submission

Submitted (22-NOV-2000) to the DDBJ/EMBL/GenBank databases. Takeshi Yamagami, Kyushu University, Protein Chemistry and Engineering, Faculty of Agriculture: Hakozaki, 6-10-1, Fukucka, Higashi-ku, Fukucka 812-8581, Japan (E-mail:yamagami@uclink.berkeley.edu, Tel:81-92-642-4218, Fax:81-92-642-3051)
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/product="seed chitinase-a"
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GNTSDYCGTGCOSOCNGCSGPTPVPFPSGGGGVSSIVSQS.LFBQMLLHRNDPSCQAN
GFYTXAFILAANSFAGFTGSTDVRKREVABLAGTGFFTGGWPTADGPFSWGY
CYRQEQGATSDYCSPSSQWPCAPGKRYFGRGPTQISFNYNYGPAGQALQTDLLNNPDL
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(Dases 1 to 1252)
Du,M. and Ha,S.B.
Direct Submission
Submitted (22-APR-1997) Plant Biology, U.C. Berkeley, Berkeley,
                                963
          894
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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/organism="Poa pratensis"
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/protein_id="AAF04453.1"
/db_xref="G1:6164585"
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(Chil)
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28. .1050
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Poa pratensis chitinase
AF000964
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/gene="Chi1"
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73.9%;
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Submitted (11-MAY-1993) to the DDBJ/EMBL/GenBank databases. Yoko
Nishizawa, National Institute of Agrobiological Resources, Rice
Genome Research Program: 2-1-2 Kannondai, Tsukuba, Ibaraki 305,
Japan (E-mail:CS.SUZUKI/NFRI, Tel:0298-38-7451, Fax:0298-38-7408)
Submitted (11-MAY-1993) to DDBJ by:
                                                                                                                                                                                                486
                       400 AGCACCGACGAGGAGGCGGGGGCGGCCTTCCTCGCTCAGGACCTCCACGAGACC 459
                                                                                             367 gacctggacacgcggaagcgggaggtggcggccttcttcggccagacctctcacgagacc 426
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tacacgtacgacgccttcttggccgccgccgcgcgttcccggccttcggcaccaccgga
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Nishizawar, Y., Kishimoto, N., Saito, A. and Hibi, T. Sequence variation, differential expression and chromosomal location of rice chitinaes genes
                                                                                                                                                                                                                                                                                                                                                                                                                  880 GACAACCGCGTCGCAGTCGCAGACCGGATCGGGTTCTACAAGCGCTACTGCGACCTCCTC
                                                                                                                                                                                                accogcogggtggcccaccgcccgacggccccttctcatggggctactgcttcaagcag
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D16223.1 G1:452234
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Oryza sativa (strain Nipponbare) DNA, clone RCG3.
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Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibrarki 305-8602, Japan (E-mail:tsasaki@abraffrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7469)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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2236 TGGCGCAGACGTCCCACGAGACCACCGCGGCGGCTGGCCCCACGGCCCCGACGGCCCCTACT 2295
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                                                                             521 gegecegactegecegtegeacceggeaageagtactategecegeggececatecagetea
                                                                                                                                                                    2356 AGCCGGAGTGGCCGTGCGCCGCCGGCAGAAGTACTACGGCCGGGGACCCATCCAGATCA
                                                                                                                                                                                                             cocacaactacaactacggaccggcggcgcaatcggggtggacctgctgaacaatc
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Oryza satiya nipponbare(GA3) genomic DNA, chromosome 6,
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Ehrhartoideae; Oryzeae; Oryza.
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Direct Submission
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AP003685.1 GI:14192855
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                                                                                                                                                                                                                                                         /note="transcription initiation site"
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1833, 2795
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               Institute of Agrobiological Resources
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ilarity 73.0%; Pred. No. 5.5e-62;
Conservative 0; Mismatches 231;
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1723. .1730
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/gene="cht-3"
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/gene="Cht-3"
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               by the finished sequence as soon as it is available and
the accession number will be preserved.
Location/Qualifiers
                                                                                                                                                                                                Similarity 73.0%; Pred. No. 9.5e-63; Similarity 73.0%; Pred. No. 9.5e-63; Onservative 0; Mismatches 231; Indels 30;
                                                                                                                                             400 others
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This sequence will be replaced by the finished sequence as soc
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SYCKERNOWSDYGYQSSQWPCAAGKKYYGWEDJQISYNYXYGPAGQAIGSNILSN
PDIVASDATVSFKPEWFWMPGOSPKPSCHAYMTGWTPNGNDAAGRYPGYGYTNI
INGGVECGHGADSRVADRIGFYKRYCDMLGVSYGANLDCYNQRPFNS'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (11-MAY-1993) to the DDBJ/EMBL/GenBank databases. Yoko
Nishizawa, National Institiute of Agrobiological Resources, Rice
Genome Research Program: 2-1-2 Kannondal, Tsukuba, Ibaraki 305,
Japan (E-mail:Cs.SUZUKI/NFRI, Tel:0298-38-7451, Fax:0298-38-7408)
Submitted (11-MAY-1993) to DDBJ by:
                                                                                                                           19170 AGCGTACTGCGACATGCTGGGCGTCAGCTATGCGGATACCTGGATTGCTACAGCAGA 19111
                                 19230 GCGGTGTGCAGGCGCACGCGCGGACGACGTGGCCGACCGGATCGGGTTCTACA 19171
                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-2000
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I (basea I to 2739)

I (shizawa,Y., Kishimoto,N., Saito,A. and Hibi,T. Sequence variation, differential expression and chromosomal location of rice chitinase genes

MOL Gen. Genet. 241 (1-2), 1-10 (1993)
gcgggatccaatgcggcatggggcagaacgacaaggtggcggatcggatcgggttctaca
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Tsukuba, Ibaraki 305
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1318. .2289
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Nishizawa,Y.
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1 (bases 1 to 1151)
Zhu.Q. and Lamb.C.J.
Plant defense genes and plant defense regulatory elements
Patent: US 569593-A 2 09-DEC-1997;
Location/Qualifiers
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Pred. No. 7.5e-59;
0; Mismatches 234;
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al Similarity 72.4%;
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3, 2002, 16:32:02 ; Search time 309.71 Seconds (without alignments) 2690.647 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Rye chitinase-like	RCH10 chitinase qe	Rice chitinase RCH	Nucleotide sequenc	cDNA encoding a ma	Sequence encoding	Floral organ-speci	Seguence encoding	Chitinase coding s	Full length chitin	American elm chiti
SUMMARIES	AAX24889	AAQ31408	AAQ81346	AAF54983	AAA96224	AAQ62518	AAV49982	AAQ05264	AAT79940	AAT79941	AAT33325
DB	20	13	16	22	21	15	19	11	18	18	17
% Query Match Length DB	954	1151	1151	3035	1163	1002	1318	4704	879	866	1225
% Query Match	55.9	51.1	51.1	51.1	50.8	48.3	42.B	40.8	38.6	38.6	38.1
Score	543.4	496.6	496.6	496.6	493.4	469.4	416.2	396.2	375	375	370
Result No.	П	7	е	4	Ŋ	9	7	80	on	10	11

Banana ripening fr Tobacco intracellu Nicotiana sp. intr cDNA sequence enco Rye chitinase-like Banana fruit ripen	fruit r fruit r fruit r ncoding	CDNA encoding a ma Banana fruit ripen Banana fruit ripen Arabidopsis thalia PR-O CDNA CLONEd i	Tobacco PR-0 gene. Tobacco PR-0 gene. PR-0 protein encod Floral organ-speci CDNA encoding a ma	dioica a extrac a hybrid equence fruit r	Tobacco PR-P gene PR-P protein encod cDNA encoding a ma cDNA encoding a ma Sequence encoding Endochitinase prec
AAX25613 AAQ12898 AAT89952 AAA58910 AAX24890 AAV69461	AAA96233 AAV69463 AAV69462 AAA96231 AAA96230	AAA96234 AAV69464 AAV69466 AAC41918 AAO06185	AAV62809 AAV72995 AAV49983 AAA96227		AAV62813 AAV81601 AAA96237 AAA96232 AAQ21007 AAQ68352
70 70 70 70 70 70 70	21 20 21 21	20 20 21 21	77,000,000	1221	20 20 21 21 13
7397 1152 1152 1152 756 721	1118 755 802 1013	583 769 768 991 1010	1020 1020 1020 2636 1619	1317 1317 965 966 730 968	968 1116 1048 1153
34.7 32.6 32.6 32.6 31.3		27.3 24.5 23.3 21.1	2002 2002 1000 1000 1000 1000 1000 1000	118.88 118.88 118.88 118.20	18.0 18.0 17.1 16.8 16.6
337.6 316.8 316.8 316.8 304.2	296.4 289 285.4 278.6	265.2 238 226.2 205.2 196	196 196 197 1986 186	185.6 183 183 183 176.8	175.2 175.2 166.4 163.2 161.6
13 14 15 16	18 19 20 21 22	222 222 265 26	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 4 4 4 0 4 5 6 4 6

ALIGNMENTS

RESULT

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CHT9; chitinase-like protein; antifreeze protein; AFP; winter rye; antifungal; fungicide; cold tolerance; frost tolerance; transgenic plant; preservation; cryopreservation; tumour; therapy;
                                                                                                                                                                        1..954
/*tag= a
//ote= "separately claimed in Claim 2"
1..60
/*tag= a
61..954
/*tag= b
                                                                                                                                                                                                                                            /note= "separately claimed in Claim 2"
                                                                       Rye chitinase-like protein CHT9 cDNA clone ch-9.
                                                                                                                                                               Location/Qualifiers
           AAX24889 standard; cDNA; 954 BP
                                                                                                                                                                                                                                                                                                          98WO-CA00745.
                                                                                                                                                                                                                                                                                                                             97US-0903872.
                                                  21-JUN-1999 (first entry)
                                                                                                                                           Secale cereale
                                                                                                                                                                                                                                                                  W09906565-A2
                                                                                                                                                                                                                                                                                                         31-JUL-1998;
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                                                                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                                                     11-FEB-1999
                                                                                                                                                                                                                            mat_peptide
                               AAX24889;
AAX24889
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AAQ31408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes winter rye (Secale cereale L. cv. Muskateer) CHT9 preprotein (see AAW98079). Mature CHT9 (see AAW98080) is a chitimase-like protein that has chitimase (antifungal) and antifreeze activities. CHT9 cDNA (ch-9) was obtained by isolating mana from rye plants grown at low temperatures in the absence of pathogens or other stresses, i.e. under conditions when only chitimases with antifreeze activity would be expressed, and then sorting the cold-induced chitimase cDNAs to determine which encoded proteins with ice-binding ability. CHT9 and CHT46 (see AAW98081-82) corting the cold-induced chitimase cDNAs to determine which encoded proteins with ice-binding ability. CHT9 and CHT46 (see AAW98081-82) corting the cold-induced chitimase cDNAs to determine which encoded systems and in Arabidopsis thaliana. The chitimase-like antifreeze proteins can be used: to increase freezing tolerance of plants and microorganisms; to increase field survival of plants, animals and microorganisms exposed to sub-zero temperatures; to inhibit ice cryptablisation in biological materials or foods; for cryptorservation and hypothermic protection of cells, embryos, tissues etc. (particularly human plantelets) is and too kill tumour cells. They are also used to inhibit initiation and progression of diseases or spoilage caused by low temperature pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                 New nucleic acid encoding antifreeze polypeptides from plants -
particularly with chitinase activity, used to impart frost, and
pathogen, resistant to plants, for preservation of foods, cells etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtoctggccgtcgtcctggcggcggcgggtcacgccggccacggccgagcagtgcggc 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 accgacgtcaggaagcgcgaggtggccgcgttcctagctcagacctcccacgagaccacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.9%; Score 543.4; DB 20; Length Best Local Similarity 75.0%; Pred. No. 3e-86; Matches 704; Conservative 0; Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 954 BP; 162 A; 335 C; 306 G; 151 T; 0 other;
                                               Xiong F;
                                                                                                                                                                                            Claim 2; Fig 21a; 118pp; English.
                                            Moffatt B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (particularly fungi) in plants, biological material.
                                                                       WPI; 1999-153795/13.
P-PSDB; AAW98079, AAW98080.
                                                                                                                                                               and for treating tumours
              (ICEB-) ICE BIOTECH INC
                                            Hew C,
                                         Griffith M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213
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493 egeggegeececteegactactgetegeegagetegeagtggeegtgegeggggeaag 552
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433 99c9g9tggcccacggcgcccgacggcccctactcgtggggctactgcttcaaccaggag 492
                                                                                                                                              550 cagtactatggccgcggccccatccagctcacccacaactacaactacggaccggcgggc 609
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                                                                                                                                                                    /*tag= d
/note= "Region conserved between class I and class
II chitinases"
                                                                cagggctcgccgaccgaccagagcgccgactggccgtgccgtgccggcaag
                                                                                                                                                                                                                                cgcgcaatcggggtggacctgctgaacaatccggacctggtggccacggacccgacagtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leaves; stems; roots; male; female; reporter; monocotyledon; dicotyledon; development; plant; defence; selectable; genes; ss.
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/note= "Putative polyadenylation signal"
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/note= "Putative polyadenylation signal"
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DNA fragment contg. chitinase gene and its regulatory region - is responsive to mature plant stress and has low level expression in leaves, moderate level expression in stem and high level expression in roots
                                                                                                                    Disclosure; Page 33-34; 45pp; English.
       (SALK ) SALK INST BIOLOGICAL STUDIES.
                                            WPI; 1992-415785/50.
                                                   P-PSDB; AAR29019
                          Zhu Q;
                          Lamb CJ,
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The sequence given represents the rice chitinase gene. The promoter region of this gene (see AA031407) is responsive to physical and/or biological stress. The pattern of expression of this gene in mature plants is characteristic. There is a low level of expression in leaves, a moderate level in plant stems and the highest level in roots and the male and female parts of the plant. The chitinase promoter sequence may be linked to a reporter gene for expression in mono- or dicotyledon plants. Expression of this reporter gene may be used to study patterns of development and controlled expression of plant defence genes and selectable genes.

Sequence 1151 BP; 197 A; 409 C; 353 G; 192 T; 0 other;

ä 200 236 57 gagagogotogotgiggiggocatggiggocaggocottootogoggoggoggoatgcatgc 116 cgagcagtgcggctcgcaagccggcggcgaccaagtgcgccgactgcctgtgctgcagcca 140 296 356 356 357 cagcaacttctacacctacgacgccttcgtcgccgccgccagcgccttcccgggcttcgc 416 caccaccygagacctygacacycygaagcygygaggtygcygcettetteggecagacete 416 536 cttcaagcaggagca---gggctcgccgagctactgcgaccagagcgccgactggcc 533 80 Gaps 9ttcgggttctgcggcaccacctccgactactgcggccccgctgccagagccagtgcac 177 gitiogotiggigogoticcacciccgactactgoggogocoggatgocagagocagtgotc .----tagotacagtagoggoggogggggtagoctocat cgtgtccagggacctcttcgagcggttcctgctccatcgcaacgacgcagcgtgcctggc cogogggettetacacgtacgacgcettettggccgccgccggcggcgttcccggccttcgg 477 ccacgagaccaccggcgggtgggcgacggcgcccgacggccctacacgtggggctactg 537 cttcaaggaggagaacggcggcggccggactactgccagcagagcgcgcagtggcc gigogocgccgccaagaagiactacggccggggtcccatccagctctcctacaacttcaa 1151; 27; Length Indels DB 13; 234; Score 496.6; DB 13 0; Mismatches 51.18; 72.48; Local Similarity '2.* hes 684; Conservative Query Match Best Loca Matches 201 81 237 297 297 357 477 534 597 OD $\overset{\circ}{\Delta}$ qq Db δà ð òγ Q_{Y} q Qγ g δλ q δy a ΩĎ Qγ δy

The SphI fragment of rice chitinase RCH10 gene (given in AAQ81346) and an alfalfa beta-1,3-glucanase coding sequence (AAQ81347) were incorporated into vectors for co-expression in transgenic tobacco, resulting in improved resistance to Cercospora nicotinae and ctacgggccggcgggggggggcatcggcgacctgctcggcgacccggacctcgtggc 716 cacggaccegacagtggcgttcaagacggcgatatggttctggatgacgacgcagtccaa 713 caagecgtegtgecatgaegtgateaeggggetgtgggaeteegaeggeeagggatagege 773 ctacggaccggcggcgcgatcggggtggacctgctgaacaatccggacctggtggc agccggacgggtacccggggtatggtgtcatcaccaacgtcatcaacggcgggatccaatg eggecatggegaggaegategeategeegaeeggateggettetaeaagegetaetgega when Chitinase, RCH10 gene, transgenic plant; disease resistance, crop improvement; tobacco, Nicotiana tabacum; plant defense; associated pathogens w cattttcggcatcggctacgggaataacctcgactgctacaacca several plant defence ed resistance to plant Thanatephorus cucumeris fungal infection crop improvement; tobacco; Nicotiana ti fungus pathogen; Cercospora nicotinae; Disclosure; Page 31-32; 45pp; English. STUDIES Location/Qualifiers 55..1065 /*tag= a grown in crops as a food source Maher EA, CDNA; 1151 (SALK) SALK INST BIOLOGICAL 93US-0093372. 94WO-US07815 Thanatephorus cucumeris; ss Transgenic plants contg. se proteins - have increased (first entry) Rice chitinase RCH10 gene Lamb CJ, WPI; 1995-067090/09 standard; P-PSDB; AAR67969 Oryza sativa 15-JUL-1994; 16-JUL-1993; 13-AUG-1995 WO9502319-A 26-JAN-1995 Dixon RA, AAQ81346 AAQ81346; 177 837 897 957 594 657 654 714 774 834 894 AAQ81346 gg qq qq q $\vec{0}$ δž δ g ă q Qγ BP

(first entry)

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Disease resistance protein; Xa21; RKK gene; transgenic plant; chitinase; Xanthomonas; plant pathogen; Bril protein; RCH10 protein; ss.
                                                               Nucleotide sequence of a rice chitinase designated RCH10
           AAF54983 standard; DNA; 3035
                                              15-MAY-2001
                              AAF54983;
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353 G; 192 T; 0 other;
                           16;
                          Score 496.6; DB 1 Pred. No. 3.9e-78;
                                            0; Mismatches
Sequence 1151 BP; 197 A; 409 C;
                          51.18;
72.48;
                                           684; Conservative
                                   Similarity
                           Query Match
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The present sequence encodes a chitinase designated RCH10. The specification describes chimeric receptors which are used for modulating plant responses to pathogens. The receptors comprise a heterologous extracellular domain (e.g. from a Bril protein or RCH10 protein) and a kinase domain (e.g. from disease resistance protein Xa21). The Xa21 gene is a member of disease resistance genes referred to as RKK genes. When Xa21 is present in a transgenic plant, it confers resistance to Xanthomonas spp.. The plant receptors containing heterologous domains are useful for modulating plant responses to pathogens including viruses, bacteria, nematodes, fungi or insects. The nucleic acids can be used to
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Pred. No. 3.7e-78;
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The present sequence encodes a chitinase polypeptide. The specification describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896, AAB18895, and AAB18902-05), and glucosyl hydrolase famiy 18 chitinases (AAB18895, AAB18897-98 and AAB18900-01). The level of chitinase in plants can be modulated to enhance disease resistance in crop plants and for control of pathogens. The chitinase polynucleotides are also useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 catggggctactgcttcaagcaggagcagggc----tcgccgccgagctactgcgacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1163 BP; 231 A; 391 C; 358 G; 183 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 493.4; DB 21;
Pred. No. 1.4e-77;
0; Mismatches 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cttcggcaccaccggagacctggacacgcggaagcgggag
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                                                                                                                             (PION-) PIONEER HI-BRED INT INC
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Best Local Similarity 74.1%;
Matches 678; Conservative (
                                                                                             99US-0125915
                                                             09-MAR-2000; 2000WO-US06121
                                                                                                                                                                                         2000-628269/60
                                                                                                                                                                                         WPI; 2000-628269
P-PSDB; AAB18896
                                                                                             24-MAR-1999;
                               28-SEP-2000
                                                                                                                                                           Simmons CR,
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                  tatectacaactacaactacgggcccggccaggccatcggcgccggcatcctcgcca
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/note= "Putative polyadenylation signal."
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                                                                                    This sequence encodes Chitinase G. Chitinase is an enzyme which breaks down chitin, the major protein in insect exoskeletons. The coding sequence may be used in the construction of transgenic organisms, especially plants, to produce pathogen resistant organisms. The genome of such transgenic organisms preferably contains more than one gene with pathogen inhibiting activity, each gene under the control of active promoters. The two gene products then show a synergistic increase in pathogen induced activity so th
                                                                                                                                                                                                                                                                                                                                                                                geggttectgetecategeaaegaegeagegtgeetggeeegegggttetaeaegtaega
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                                                                                                                                                                                                                                                                                                                             cactggctgcggtggcggcggcggcggggtggcctccatcgtgtccagggacctcttcga
contg. at least 2 pathogen inhibiting genes genes with antifungal activity, show in disease resistance, also new DNA transfer
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                                                                                                                                                                                                                                                                             Length 1002;
                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                            the transgenic organisms have a greater degree of resistance resistance against a wider spectrum of diseases.
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                   Sequence 1002 BP; 194 A; 329 C; 293 G; 186 T; 0 other;
                                                                                                                                                                                                                                                                         Score 469.4; DB 15;
Pred. No. 2.1e-73;
); Mismatches 176;
                                                            Example 2; Page 13-14; 19pp; German
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Transgenic organisms - esp. plants contg. synergistic increase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This cDNA encodes a floral organ-specific chitinase. The specification provides a promoter sequence (AAV49983) derived from rice associated with chitinase, specific to floral organs that allows expression of genes in the flower parts of monocotyledonous plants. The expression of desired genes specifically in the floral parts of monocotyledonous plants, allows modifications to be made in the structure or function of these parts allowing the introduction of desired characteristics such as increased resistance to bacterial attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caageeggeggegaagtgegeegactgeetgtgetgeagecagtteggggttetgegge 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific gene; chitinase; promoter; Oryza sativa; rice; monocotyledonous plant; bacterial resistance; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Promoter sequence associated with chitinase, specific to floral organs - allows expression of genes in the flower parts of monocotyledonous plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.8%; Score 416.2; DB 11
Similarity 68.4%; Pred. No. 3.5e-64;
4; Conservative 0; Mismatches 233
                                                                                                                                     Floral organ-specific chitinase encoding cDNA
 taacctcgactgctacaaccaattgtcgttc 948
                   828 caacctcgattgctacagccagagacccttc 858
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                                                                                                                                                                                                               Location/Qualifiers
114..1100
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                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                      (NISB ) JAPAN TOBACCO INC
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P-PSDB; AAW64776.
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hes 674;
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us-09-534-229c-7.rng

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Sequence 879 BP; 216 A; 221 C; 242 G; 200 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                          1 40.8%; Score 396.2; DB 11; Length 4704; Similarity 67.2%; Pred. No. 9.6e-61; 76; Conservative 0; Mismatches 278; Indels 3;
                                                                                                                                                                                   Recombinant DNA contg. high level promoter and plant chitinase gene - for transforming plants to over:express chitinase, imparting resistance to phytopathogenic fungi.
                                                                                                                                                                                                                                             Sequence encoding chitinase may be used to transform monoor dioctyledons to show increased resistance to fungal attack. A high level promoter is used from CMV 35s or 19s complement, NOS or OCS promoters of Agrobacterium opine synthetase gene, the RUBISCO small unit or the chlorophyl A/B binding protein.
                                                                                                                                                                                                                                                                                                            Sequence 4704 BP; 1528 A; 783 C; 872 G; 1521 T; 0 other;
                                                                                                              (DUPO ) DU PONT DE NEMOURS CO
                                                                                          88US-0285252
                                                                       89WO-US05501
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                                                                                                                                                              P-PSDB; AAR05931
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This sequence represents the coding sequence for the pumpkin chitinase. Chitinase is an enzyme decomposing chitin (not present in plant cell membranes) found in the cell membranes of fungi. Plants have this enzyme to protect themselves from pathogenic fungi. Thus this enzyme can be used to prevent plants from being infected with pathogenic fungi, and the chitinase gene can be introduced into plants to improve their resistance to diseases caused by fungi. As the amino acid sequence of the chitinase does not have any region to be cleaved by ubiquitous peptidases in cells, the chitinase produced by genetic recombination technology works for various host cells and serves for plant immunity to confer disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase; fungal cell membrane; pathogenic fungus; disease resistance; chitin; ss.
                                                           2670 gttgacttgctcaacaaacctgatctagtcgccactgactctgtcatctccttcaagtcc 2729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2910 gaccgcatcggattcttcaagagatactgtgatctgcttggagttggttatggcaacaac 2969
                                                                                                                                                                                     862 gatcggatcgggttctacaaagcgctattgtgacattttcggcatcggctacgggaataac 921
gtggacctgctgaacaatccggacctggtggccacggacccgacagtggcgttcaagacg
                                                                                                                                                                                                                                                                                       742 gggetgtggaetecgaeggeeagggatagegeageeggaegggtaeeegggtatggtgte
                                                                                                                                                                                                                                                                                                                                                                  2790 totogatggaccocctcctctgccgacgtcgccgccggccggcttcccggctacggcact
                                                                                                                                             gegatatggttctggatgacgacgcagtccaacaagecgtcgtgccatgacgtgatcacg
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us-09-534-229c-7.rng

Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase; fungal cell membrane; pathogenic fungus; disease resistance; chitin; ss.

/product= chitinase

JP09163987-A

24-JUN-1997

/*tag= 1..879

95JP-0347367 95JP-0347367

14-DEC-1995; 14-DEC-1995;

Location/Qualifiers

Cucurbita pepo.

Full length chitinase coding sequence

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                                                                                                                   142 ttcgggttctgcggcaccacctccgactactgcggccccgctgccagagccagtgc--- 198
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                                                                                                                                                                                  cccccagtaccggcggcggcggcggcggcagcgttggaagtatcatcaacgaagcc 180
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 Length 879;
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                          285;
Score 375; DB 18;
Pred. No. 5e-57;
                        0; Mismatches
38.6%;
65.9%;
                       581; Conservative
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Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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(SEKI-) ZH SEKIYU SANGYO KASSEIKA CENTER
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(first entry)

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Matches
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                      ggcgggtggcccaccgcgccgacggcccttctcatggggctactgcttcaagcaggag
                                                                                          419 -agagaaaccaagacgtatattgctcacctaaccagcaatggccgtgtgctgctggccag
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                                            361 ggagggtgggctacggcaccggatggcccatatgcgtggggatattgcttcataaggg--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone pHS2; chitinase; american elm; fungus; Ophiostoma dutch elm disease; E. coli; chitinase-like protein; fungal infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   American elm chitinase-like protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                           tacgggaataacetegaetgetacaaecaattgtegtteaa 950
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88..150
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/product= C
1147..1151
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151..1038
/*tag= b
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/*tag= d 1153..1158 /*tag= e 1168..1177 /*tag= f

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AAT 3325

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US5539095-A. 23-JUL-1996

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This sequence represents the cDNA clone pHS2, which encodes a protein having chitinase-activity derived from american elm. This protein inhibits the fungus Ophiostoma ulmi, the causative agent of dutch elm disease. The clone pHS2 may be used to transform E. coli cells for the recombinant production of the chitinase-like protein. The protein may be used in a composition to inhibit fungal infection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gecaeggeegageagtgeggetegeaageeggeggegeeaagtgegeegaetgeetgtge 132
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                                                                                                                                                                                                                              Isolated chitinase gene derived from an American obtain prods. for inhibiting fungal infection of
                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1; 12pp; English
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al Similarity 64.4%;
572; Conservative (
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                                                                                                                          aaggtggcggatcggatcgggttctacaagcgctattgtgacattttcggcatcggctac 912
                                  gtgatcacggggctgtggactccgacggccagggatagcgcagccggacgggtacccggg
                                                                                          913 gggaataacctcgactgctacaaccaattgtcgttcaacgttgggctc
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AAX25613 standard; DNA; 7397 BP Banana ripening fruit Endo. DNA (first entry) 02-AUG-1999 AAX25613; AAX25613 RESULT

Banana; fruit ripening; differential expression; fruit development; transgenic plant;

Musa acuminata.

W09915668-A2

01-APR-1999

98WO-US03343 23-SEP-1998;

97US-0060062 25-SEP-1997;

(BOYC-) BOYCE THOMPSON INST PLANT RES

Clendennen S, May G;

P-PSDB; AAY05842, AAY05843, AAY05844 WPI; 1999-244425/20

New isolated banana DNA molecules

Claim 5; Fig 16A-J; 143pp; English

This is the nucleotide sequence of a DNA molecule termed ENDO. The invention provides isolated DNA molecules which are differentially expressed during banana fruit development, and the protein products of these genes. The DNA is selected from a group comprising starch traumatin-like protein, ascorbate peroxidase, metallothionein, the genes can be used to produce chimaeric genes for transformation the genes can be used to produce chimaeric genes for transformation of plants to provide controlled expression of heterologous DNA curing fruit development, or in response to exogenous developmental signals, such as ethylene signals. The heterologous protein, e.g. a therapeutic protein, can be isolated from the fruit or consumed directly in the transformed fruit. The identity of the present sequence is not given. The entire DNA sequence has been decoded in all 3 reading frames to provide the amino acid sequences given in

Sequence 7397 BP; 2109 A; 1549 C; 1592 G; 2012 T; 135 other;

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5396 ggaggatgaaggeettgttgetggteatttttaeeettggeetegtegeteggegeetteg 5455
                                                                                                                                                                                                        5516 agtacggctggtgcggtaacacggatccatnctgcggtcaaggatgccananccaatgcn 5575
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                                                        20 ggtgtgcgacggccgtcctggccgtcgtcggcggcggcggcggccacggccacgg
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   Length 7397;
Score 337.6; DB 20; Length
Pred. No. 1.4e-50;
); Mismatches 302; Indels
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34.78;
61.58;
               Best Local Similarity 61.5
Matches 626; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 ctgcctcggcagaacaatgtggttcgcaggcgggaggtgcgcgttgtgcctcgggtctct 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 agagecagtgecetggtggteceacaecacceggtggtggggateteggeagtateatet 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccagggacctcttcgagcggttcctgctccatcgcaacgacgcagcgtgcctggcccgcg 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was isolated from a N.tabacum cDNA library following screening with a partial tobacco intracellular chitinase clone. The gene can be inserted into an appropriate plasmid for production of transgenic plants having resistance to fungal pathogens. The sequence was modified so as to obtain apoplast targeting of the protein. G(961) was mutated to a T to create a STOP codon. A second restriction site was created by mutation of T(968) to A and a Sall sestriction site was created by changing T(975) to C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          getgeagecagttegggttetgeggeaceaecteegactactgeggeeeeege---tgee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
o
                                                                                                                                                                                                                                                                                                                                                                   contains
                                                                                                                                                                                                                                                                                                          JS;
                                                                                                                                                                                                                                                                                                        Roekel
JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                              Plants with improved resistance to pathogenic fungi - chitinase and/or beta-1,3-glucanase genes modified for over-expression targetted to apoplasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1152 BP; 281 A; 273 C; 283 G; 315 T; 0 other
                                                                                                                                                                                                                                                                                                         Van
Bol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 32.6%; Score 316.8; DB 12; Local Similarity 61.5%; Pred. No. 6.1e-47; les 545; Conservative 0; Mismatches 332; ...
                                                                                                                                                    10..984 /*tag= a /product= intracellular_chitinase
                                                                                                                                                                                                                                                                                                        Meulenhoff EJ,
Woloshuk CP,
                                                                                  intracellular chitinase gene.
                                                                                                                                             Location/Qualifiers
                                                                                                     fungal resistance; phytopathogen;
                          ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 2; 55pp; English.
                                                                                                                                                                                                                                                                                                                Vloemans AA,
                                                                                                                                                                                                                                                                                                       Melchers LS,
                         DNA; 1152
                                                                                                                         Nicotiana tabacum Samsun NN
                                                                                                                                                                                                                                                                       (MOGE-) MOGEN INT NV.
(UYLE-) RIJKSUNIV TE LEIDEN
                                                                                                                                                                                                                                   91EP-0200191
                                                                                                                                                                                                                                                     90NL-0000222
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                   1991-232019/32.
                       AAQ12898 standard;
                                                                                                                                                                                                                                                                                                                Sela-Buurlage MB,
                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAR13275.
                                                                                                                                                                                                                                                                                                     Cornelissen BJ,
                                                                                                                                                                                                                                   30-JAN-1991;
                                                                                                                                                                                                                                                     30-JAN-1990;
                                                              14-0CT-1991
                                                                                                                                                                                                                07-AUG-1991
                                                                                                                                                                                            EP440304-A.
                                           AAQ12898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                  Tobacco
      13
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Matches
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               AAQ12898
      RESULT
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307
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                                                                                                                              421
                                                                                                                                                                                                                 agaccaccggcgggtggcccaccgcgcccgacggcccttctcatggggctactgcttca 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgtgccatgacgtgatcacgggggctgtggactccgacggccagggatagcgcagccggac 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              848 gcactgactcaagggtccaggatcgcattgggttttacaggaggtattgcagtattcttg 907
ggttctacacgtacgacgccttcttggccgccggcggcggcgttcccggccttcggcacca
                                                                                                                                                                                                                                                 aaactacaggaggatgggcaacagcaccagatggtccatacgcgtggggttactgctggc
                                                                                                                                                                                                                                                                                                482 agcaggagcagggetegeegeegagetactgegaecagagegeegaetggeegtgegee
                                                                                                                                                                                                                                                                                                                           ccggcaagcagtactatggccgcggccccatccagctcacccacaactacaactacggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cggcgggccgcgcaatcggggtggacctgctgaacaatccggacctggtggccacggacc
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                                                                                                                            ccggagacctggacacgcggaagcgggaggtggcggccttcttcggccagacctctcacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Intracellular chitinase; antifungal; transgenic plant; synergism;
beta-1,3-glucanase gene; tobacco; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    902 gcatcggctacgggaataacctcgactgctacaaccaattgtcgtt 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  908 gtgttagtcctggtgacaatcttgattgcggaaaccagaggtcttt 953
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10..78
/*tag= b
79..981
/*tag= c
/product= intracellular_chitinase
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661

787 841

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New transgenic plants expressing chitinase and glucanase have improved resistance against pathogenic fungi, particularly against Alternaria alternata or Fusarium oxysporum f. sp. lycopersici
                                                                                                             cagtaatctcattcaagtcagctctctggttttggatgactcctcaatcaccaaaacctt 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sela-buurlage MB;
M, Van Roekel JSC;
ctggtcggaaatatttcggacgaggccccatccaaatttcacacaactacaactacggac
                            cggcgggccgcgcaatcggggtggacctgctgaacaatccggacctggtggccacggacc
                                          cgacagtggcgttcaagacggcgatatggttctggatgacgacgcagtccaacaagacgt
                                                                                                                                           cgtgccatgacgtgatcacggggctgtggactccgacggccagggatagcgcagccggac
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                                                                                                                                                                                                                                                          ggcagaacgacaaggtggcggatcggatcgggttctacaagcgctattgtgacattttcg
                                                                                                                                                                                                                                                                         Chitinase; transgenic plant; beta-1,3-glucanase; antifungal; plant resistance; pathogenic fungi; fungal resistant plant; ss.
                                                                                                                                                                                                                                                                                                                  947
                                                                                                                                                                                                                                                                                                                                 gcatcggctacgggaataacctcgactgctacaaccaattgtcgtt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA sequence encoding an extracellular chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meulenhoff EJS,
JF, Linthorst H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cocation/Qualifiers
10..984
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                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Melchers LS,
oshuk CP, Bol
                                                                                                                                                                                                                                                                                                                                                                                                                   AAA58910 standard; cDNA; 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0047413,
91US-0647831,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0801563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDE; AAB07513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-1991;
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                                                                                                                                                                                                                                                                                                                              to construct a transgenic plant in a novel method to produce plants resistent to fungal attack. Such transgenic plants expressing an intracellular plant chitinase gene and a plant beta-1,3-glucanase gene within its tissues are predicted to exhibit improved resistance to pathogenic fungi. Such genes should be operably linked to promoters and terminators and optionally a gene encoding a selectable or screenable trait. Plants that overexpress the chitinase and glucanase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                  cDNA sequence encodes an intracellular chitinase which is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggttetacaegtaegaegeettettggeegeeggeeggetteeeggeetteggeaeea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1152;
                                                                                                                                                                                                                                            genes encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1152 BP; 281 A; 273 C; 283 G; 315 T; 0 other;
                                                                                                                                          Linthorst HJM, Melchers
1ge MB, Van ROEKEL JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 316.8; DB 18;
Pred. No. 6.1e-47;
0; Mismatches 332; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               containing
                                                                                                                                                                                                                                           Fungus-resistant transgenic plants - containing intracellular chitinase and beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                 exhibit a synergistic antifungal effect.
                                                                                                                                                       S, Sela-buurlage MB,
Woloshuk CP;
                                                                                                                                                                                                                                                                                     Example 4; Fig 2; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.6%;
llarity 61.5%;
Conservative
                                       93US-0047413
                                                                    91US-0647831
                                                                                                                                           Cornelissen BJC,
                                                                                                          RIJKSUNIV LEIDEN
                                                                                                                                                                                               WPI; 1997-479536/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 545; Conserv
                                                                                               (MOGE-) MOGEN INT
                                                                                                                                                                                                              P-PSDB; AAW31297
                                                                                                                                                         EJS,
                                                                                                                                                                        Vloemans AA,
                                       19-APR-1993;
                                                                    29-JAN-1991;
             23-SEP-1997
                                                                                                                                                         Meulenhoff
                                                                                                              UXLE-)
                                                                                                                                        Bol JF,
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The present sequence encodes an extracellular chitinase. The specification describes transpenic plants which express a chitinase gene and a glucanase gene. The expression of the chitinase and beta-1,3-glucanase genes produces an antifungal effect. The transgenic plants are useful for improving plant resistance to pathogenic fungi. The recombinant polynucleotides and the process are useful for producing fungal resistant plants.
55555555X8
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Sequence 1152 BP; 281 A; 273 C; 283 G; 315 T; 0 other;

Query Match

Length 1152;

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2
                                                                71 cggccacggccgagcagtgcggctcgcaagccggcggcgacggcgactgcctgt 130
                                                                                                                                                                                                       241
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Score 316.8; DB 21; Length
Pred. No. 6.1e-47;
0; Mismatches 332; Indels
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32.6%;
61.5%;
                 Local Similarity 61.5 es 545; Conservative
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3, 2002, 16:32:50 completed: May e: 7004 sec Search comp Job time:

Appl Appl Appl Appl Appl Appl

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Sequence 2, Application US/07704288C
Patent No. 5399680
GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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SORTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: 22-MAY-1991
CLASSIFICATION: 800
CLASSIFICATION: 800
NAME: Release Ketter, Stephen E.
REGISTRATION NUMBER: 31,192
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llarity 72.4%; Pred. No. 1.9e-88;
Conservative 0; Mismatches 234
              US-09-350-600-7
US-08-1931-1
US-08-229-050-8
US-08-229-050-8
US-08-181-271A-12
US-08-449-315-12
US-08-449-043-12
US-08-455-416-12
US-08-455-416-12
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US-08-455-364-12
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US-08-456-262-12
US-08-456-262-12
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US-08-456-262-12
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                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEPAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 444 South Flower
CITY: Los Angeles
STATE: California
COUNTRY: United States
ZIP: 90071-2921
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 base pairs
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              COMPUTER READABLE FORM:
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Matches 684; Conserv
MEDIUM TYPE:
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3, 2002, 16:26:33 ; Search time 142.45 Seconds (without alignments) 1545.361 Million cell updates/sec
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Sequence 10,
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              Gencore version 4.5 (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Sequence 1, Application US/08093372 Patent No. 5530187 GENERAL INFORMATION: APPLICANT: Lamb, Christopher J. APPLICANT: Zhu, Qun

US-08-093-372-1

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cgagcagtgcggctcgcaagccggcggcgccaagtgcgccgactgcctgtgctgcagcca 140
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APPLICANT: Maher, Eileen A.
APPLICANT: Maher, Eileen A.
TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING MULTIPLE
TITLE OF INVENTION: DISEASE RESISTANCE GENES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,372
FILING DATE: 16-JUL-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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OTHER INFORMATION: /product= "RICE CHITINASE"
                                                                                                          ADDRESSEE: Pretty, Schroeder, Brueggemann & STREET: 444 South Flower Street, Suite 2000 CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.1%; Score 496.6; DB 1 ilarity 72.4%; Pred. No. 1.9e-88; Conservative 0; Mismatches 234
                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                           31,192
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                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 90071-2921
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tcacgagaccaccggcggggggggcccaccgcgccgacggcccttctcatggggctactg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLANT DEFENSE GENES AND PLANT
DEFENSE REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31,192 REFERENCE/DOCKET NUMBER: P31 8899 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DAIE: 22-MAX-1991
ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: EHU, QUN
TITLE OF INVENTION: DEFENSE
TITLE OF INVENTION: DEFENSE REGUI
TITLE OF INVENTION: BEENENE REGUI
TITLE OF INVENTION: BEENENTS
NUMBER OF SEQUENCES: 26
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Patent No. 5695939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90071-2921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-379-259-2
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57 GAGAGCGCTCGCTGTGGTGGCCATGGTGGCCAGGCCCTTCCTCGCGGCGGCGGCGTGCATGC 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cgtgtccagggacctcttcgagcggttcctgctccatcgcaacgacgcagcgtgcctggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | || CAGCAACTICTACACACCTACGACGCCTTCGTCGCCGCCCCCCCAGCGCCTTCCCGGGCTTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caccacoggagacotggacacgoggaagoggaggtggcggccttcttcggccagacotc
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                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                    Score 496.6; DB 1;
Pred. No. 1.9e-88;
0; Mismatches 234;
                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                    Query Match 51.1%;
Best Local Similarity 72.4%;
Matches 684; Conservative (
: (619) 546-4737
(619) 546-9392
                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1151 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                         TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                             CDS
55..1062
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                ;
US-08-379-259-2
                       TELEFAX:
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; LOCATION:
US-08-457-797A-9
                        OTHER
FEATURE:
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/function= "chitinase"
/product= "26 kD preprotein of chitinase G (ChiG)"
/note= "antifungal activity, especially on
Trichoderma reesii and Fusarium sporotrichoides as
Well as Rhizoctonia solani and Botrytis cinerea."
LOCATION: 862..1002
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3' end not shown"
                                                                                                                                                                                                                                                                                                      Transgenic pathogen-resistant organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
APPLICATION NOMBRE: US/08/457,797A
FILING DATE: June 1, 1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 18,839
REGISTRATION NUMBER: 35,225
FILING PATENTIAN NUMBER: 35,225
                                                                                                                                     894 cattttcggcatcggctacgggaataacctcgactgctacaacca 938
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Transgenic pathogen-resistant or NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
TELECOMMONICATION INFORMATION:
TELEPRONE: (212) 406-2500
TELEFAX: (212) 765-2519
TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
LENGTH: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start= 64
                                                                                                                                                                                                                                   Sequence 9, Application US/08457797A Patent No. 5689045 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Hordeum vulgare
STRAIN: L.
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905..910
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 64..861
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1.63
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: 5'UTR
                                                                                                                                                                                                                                                                                                                                                                                      New York
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LOCATION:
                                                                                                                                                                                                   RESULT 4
US-08-457-797A-9
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198 cactggctggcggtggcggcggcggcgggggtggctccatcgtgtccagggacctcttcga 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 geggtteetgeteeategeaaegaegeagegtgeetggeeegegggttetaeaegtaega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 GGCTTCGTGGCGCGCGCGCGCGCTTCCGGGCTTCGGCACCGGGGAGGCCGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
OTHER INFORMATION: /note= "potential polyadenylation OTHER INFORMATION: signal"
                                                                                                                                              NAME/KEX: sig_peptide
LOCATION: 298..312
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
                                                                                             /note= "probable signal peptide
sequence"
                                                                                                                                                                                                                                                                             OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 469.4; DB 1;
Pred. No. 3.5e-83;
0; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.3%;
76.6%;
                                                     NAME/KEY: sig_peptide
LOCATION: 64..294
OTHER INFORMATION: /not
OTHER INFORMATION: sequ
FEATURE:
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NAME/KEY: sig_peptide
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Best Local Similarity 76.6'
Matches 575; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: sig_peptide
LOCATION: 607..861
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: sig_peptide LOCATION: 466..588
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133..861
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OTHER INFORMATION: /note= "p
OTHER INFORMATION: sequence"
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Matches 575; Conservative
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LOCATION: 466..588
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133..861
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; LOCATION:
US-08-812-025-9
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/function= "chitinase"
/product= "26 kD preprotein of chitinase G (ChiG)"
/note= "antifungal activity, especially on
Trichoderma reesii and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
                                                                              857
738 cacggggctgtggactccgacggccagggatagcgcagccggacgggtacccgggtatgg 797
                                                                                                                                                798 tgtcatcaccaacgtcatcaacggcgggatccaatgcggcatggggcagaacgacaaggt
                                     648 CGCCGGCCAGTGGAGCCCGTCAGGGGCTGACCGGGCCGCAGGCCGGGTGCCCGGGTTTGG
                                                                                          Transgenic pathogen-resistant organism 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFUR....
ATTORNEY/AGENT INFUR....
NAME: TEASET. ATTOIN
RECISTRATION NUMBER: 18,839
NAME: KOLe, Lisa
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: 35,225
REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
TELEPRONE: (212) 408-2500
TELEPRONE: (212) 765-2519
TELEFAX: (212) 765-2519
TELERAX: (212) 765-2519
TELERAX: (212) 765-2519
TELERAX: (212) 765-2519
TELERAX: (212) 765-2519
TELERA: (2102) 765-2519
TELERA: (2102) 765-2519
TELERA: (2102) 765-2519
TELERA: (2102) 765-2519
TELERA: SEQUENCE CANTERISTICS:
TELERGH: 1002 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Graves, Donohue and Raymond
                                                                                                                                                                                                                         918 taacctcgactgctacaaccaattgtcgttc 948
                                                                                                                                                                                                                                                  /codon_start= 64
                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08812025
Patent No. 5804184
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Brumbaugh, Graves, STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Hordeum vulgare
STRAIN: L.
                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Tr
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
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FEATURE:
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: U.S.A.
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LOCATION: 1..63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U ZIP: 10112
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                                                                                                                                                                                                                                                                                                                                     US-08-812-025-9
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STATE:
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408 CTCCTCCGACTACTGCACCCGGAGGCCAATGGCCGTGCGCCCCGGGAAGCGCTACTA 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 egecttettggeegeegeeggegtteeeggeetteggeaceaceggagaeetggaeae 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       618 cggggtggacctgctgaacaatccggacctggtggccacggaccgacagtggcgttcaa 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                end not shown"
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                                                                                 NAME/KEY: polyA_signal
LOCATION: 9505.910
OTHER INFORMATION: /note= "potential polyadenylation
OTHER INFORMATION: signal"
                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: sig_peptide
LOCATION: 298..312
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: sig_peptide
LOCATION: 607..861
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
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LOCATION: 862..1002
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3'
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                                                                                                                                                                                     NAME/KEY: sig_peptide
LOCATION: 64..294
OTHER INFORMATION: /note= "probable signal
OTHER INFORMATION: sequence"
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LOCATION: 349..379.
OCHER INFORMATION: /note= "probable signal
OTHER INFORMATION: sequence"
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588 GACGGCCATCTGGTTCTGGATGACGGCCCAGCCCCAAGCCATCGAGCCATGCTGTGAT 647
                                                                                                                                                                              tgtcatcaccaacgtcatcaacggcgggatccaatgcggcatggggcagaacgacaaggt
                                                                                                                                                                                                                                           738 cacggggctgtggactccgacggccagggatagcgcagccggacgggtacccgggtatgg
                                                                                                                                            648 CGCCGGCCAGTGGAGCCCGTCAGGGGCTGACCGGGCCGCAGGCCGGGTGCCCGGGTTTGG
                                                gacggcgatatggttctggatgacgacgcagtccaacaagccgtcgtgccatgacgtgat
                                                                                                                                                                                                   APPLICANT:
TTTLE OF INVENTION: Transgenic pathogen-resistant organism NVMBR OF INVENTION: 12
CORRESPONDENCE ADDRESS:
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COMPUTER: IPAPY disk
COMPUTER: IBAP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/138,873A
FILING DATE: AUGUST 24,1998
ATTOREX/AGRNT INFORMATION:
NAME: Tenser, Arthur
REGISTRATION NUMBER: 18,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
TELER: 238555
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             918 taacctcgactgctacaaccaattgtcgttc 948
                                                                                                                                                                                                                                                                                                                                828 CAACCTCGATTGCTACAGCCAGAGACCCTTC 858
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09138873A Patent No. 6271438
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30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kole, Lisa
REGISTRATION NUMBER: 35,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Hordeum vulgare STRAIN: L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 1002 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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ORIGINAL SOURCE:
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. U.S.A.
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1..63
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LOCATION:
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  /codon_start= 64
/function= "chitinase"
/function= "chitinase"
/product= "26 kD preprotein of chitinase G (ChiG)"
/product= "antifungal activity, especially on
Trichoderma reesii and Fusarium sporotrichoides as
Well as Rhizoctonia solani and Botrytis cinerea."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 goggttcctgctccatcgcaacgacgcagcgtgcctggcccgcgggttctacacgtacga 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 CGCATGCTTCTCCACGCAACGACGCCCTGCCAGGCCCAAGGCTTCTACACCTACGA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     egecttettggeegeegeegegegtteeeggeetteggeaceaeeggagaeetggaeae 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            geceacegegecegaeggecectteteatggggetaetgetteaageaggageagggete 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 GGCGACTGCACCGGACGGGCCTTCGCCTGGGGCTACTGCTTCAAGCAGGAACGTGGCGC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 1002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "potential polyadenylation OTHER INFORMATION: signal"
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: sig_peptide
LOCATION: 64..294
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 296.312
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
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LOCATION: 349..378
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
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                                                                                                                                                   NAME/KEX: 3'UTR
LOCATION: 862..1002
OTHER INFORMATION: /mote= "11 nucleotides at 3'
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Pred. No. 3.5e-83;
0; Mismatches 176;
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al Similarity 76.6%;
575; Conservative
                                                                                                                                                                                                                                                           NAME/KEY: polyA_signal LOCATION: 905..910
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LOCATION: 298..312
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LOCATION: 466..588
OTHER INFORMATION: /nc
OTHER INFORMATION: sec
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LOCATION: 607..861
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133..861
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INFORMATION:
                                                                                                          OTHER INFORMATION:
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; LOCATION;
US-09-138-873A-9
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73 gccaeggccgagcagtgeggetegcaagceggeggegecaagtgegeegaetgeetgtge 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 gggtggcccaccggcgcccgacggccccttctcatggggctactgcttcaagcaggagcag 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttcgagcggttcctgctccatcgcaacgacgcagcgtgcctggcccgcgggttctacacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 CAATGTGGCGCCAGCGGTAGCGATGAC----ATTGGCGGTCTCATATCAAGCTCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 TTTAATGACATGCTTAAGCATCGTAACGACGGTGGTTGTCCTGCCAAGGGGTTTTACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496 GGGTGGGCAAGTGCACCCGACGGTCCATACTCTTGGGGATACTGCTACAATAGGGAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 38.2%; Score 371.6; DB 1; Best Local Similarity 64.5%; Pred. No. 3.3e-64; Matches 573; Conservative 0; Mismatches 309;
                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
IDENTIFICATION METHOD: sequencing
OTHER INFORMATION: DNA needed for chitinase
OTHER INFORMATION: in elm.
                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: chitinase encoding DNA
                                                                                                                       Ulmus Americana
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; PUBLICATION INFORMATION:
US-08-286-020-1
                                                                                                                                                                                 DEVELOPMENTAL STAGE: HAPLOTYPE: N/A
                                                                                                                                          STRAIN: NPS 3-487 INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                      TISSUE TYPE: N/A
CELL TYPE: N/A
CELL LINE: N/A
ORGANELLE: N/A
IMMEDIANE SOURCE: N/
POSITION IN GENOME:
                        MOLECULE TYPE: DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                         HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                         FEATURE
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                                                                                                                                                                                                                                                                                                                     707
                                                                                                                                                                                                                                                                                                                                                                                                                                                           408 CICCICCGACTACIGCACCCCGAGCGCACAATGGCCGTGCGCCCCCGGGAAGCGCTACTA 467
                                     gacggcgatatggttctggatgacgacgcagtccaacaagccgtcgtgccatgacgtgat
                                                                                                                                                                                                                                                                              cacygygotygyactccyacygccaygyataycycayccygacygytacccygytatyg
                                                                                                                                                                                                                                                                                                                 648 CGCCGGCCAGTGGAGCCCGTCAGGGGCTGACCGGGCCGCAGGCCGGGTGCCCGGGTTTGG
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                                                                                                                     cggggtggacctgctgaacaatccggacctggtggccacggacccgacagtggcgttcaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08286020
Patent NO. 5539095
GENERAL INFORMATION:
APPLICANT: Masomeh B. Stlicklen and Ravindra K. Hajela TITLE OF INVENTION: A Chitinase CDNA Clone From a TITLE OF INVENTION: Disease Resistant American TITLE OF INVENTION: Blm Tree NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIF: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         828 CAACCTCGAITGCTACAGCCAGAGACCCIIC 858
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SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NURBER: US/08/286,020
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TELEPHONE: (517) 347-4100
TELERX: (517) 347-4103
TELEX: No. 5539095e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 20,
REFERENCE/DOCKET NUMBER:
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APPLICATION NUMBER:
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TYPE: Nucleic Acid
STRANDEDNESS: Singl
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Local Similarity 64.5
nes 573; Conservative
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 CELL TYPE: N/A
CELL LINE: N/A
ORGANELLE: N/A
INMEDIATE SOURCE: N/
POSITION IN GENOME:
FEATURE:
                                                                                                                                                                                             Query Match
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                                                                                                                                         736 TICAAAACGGCCTTATGGTTCTGGATGACCCCACAGTCACAAAGCCCTCGTGCCATGAC 795
                                                                           tatggtgtcatcaccaacgtcatcaacggcgggatccaatgcggcatgggggaacgac
                                                                                        853 aaggtggcggatcggatcgggttctacaagcgctattgtgacattttcggcatcggctac
                                                 976 GGGAACAATCTTGATTGCTATAACCAGAGGCCTTTTGGGAATGGACTC 1023
                                                                                                                                                                             913 gggaataacctcgactgctacaaccaattgtcgttcaacgttgggctc 960
                                                                                                                                                                                                                                                                                                        APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela TITLE OF INVENTION: A Chitinase CDNA Clone From a TITLE OF INVENTION: Disease Resistant American TITLE OF INVENTION: Elm Tree COMMER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
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                                                                                                                                                                                                                                                                    Sequence 1, Application US/08603919
Patent No. 5728382
GENERALINFORMATION:
APPLICANT: Masomeh B. Sticklen
                                                                                                                                                                                                                                                                                                                                                                                                  Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: AGER
OPERATING SYSTEM: MS-DOS 5.00
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TELECOMMUNICATION INFORMATION:
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517) 347-4103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,
                                                                                                                                                                                                                                                                                                                                                                                   Ian C. McLeod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: NO. 5728822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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EDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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MOLECULE TYPE: DNA
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ORGANISM: Ulm
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73 gecacggecgageagtgeggetegeaageeggeggegecaagtgeegaetgeetgtge 132
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64.5%; Pred. No. 3.3e-64;
live 0; Mismatches 309;
                                           LOCATION:
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NAME/KEY: chitinase encoding DNA
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Recombinant gene coding for a protein having endochitinase activity or for a precursor thereof.
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                                           13.7 AGAGCCAGTGCCCTGGTGGTCCCACACCACGGTGGTGGGGGATCTCGGCAGTATCATCT
                                                                                     242 ccagggacetettegageggtteetgetecategeaacgaegeagegtgeetggeeegeg
                                                                                                               257 GATICTACAGTIACAAIGCCTTTATCAAIGCTGCTAGGTCTTTTCCTGGCTTIGGTACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/07842165
Patent No. 5932698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: DUBDIS, Michel
APPLICANT: GRISON, Rene
APPLICANT: LEGUAY, Jean Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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STATE: VIRGINIA
COUNTRY: USA
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                                                               gggaataacctcgactgctacaaccaattgtcgttcaacgttgggctc
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 07-JUN-1995
PRION APPLICATION DATA:
APPLICATION NUMBER: US 07/842,165
FILING DATE: 01-MAY-1992
PRION APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FF91/00607
FILING DATE: 21-JUL-1991
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REFERENCE/DOCKET NUMBER: 16781/564/BEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite
CITY: Washington, D.C.
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APPLICATION NUMBER: FR 90 09460
FILING DATE: 24-3UL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              Sequence 15, Application US/08475427
Patent No. 5859340
                                                                                                                                                                                                                                                                                          APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
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                                                                                                                                                                                                                                                       Michel
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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les 546; Conserv
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APPLICANT: DUBOIS,
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Best Local S:
Matches 546
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Tue May

APPLICANT: BOJ, JOHN F.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: DETAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNCLEOTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 17 egtgecatgaegtgatcacggggetgtggaetcegaeggeeagggatagegeageeggae 781 gggtacccggggtatggtgtcatcaccaacgtcatcaacggcgggatccaatgcggcatgg 842 ggcagaacgacaaggtggcggatcggatcgggttctacaaagcgctattgtgacattttcg 902 gcatcggctacgggaataacctcgactgctacaaccaattgtcgtt 947 PatentIn Release #1.0, Version #1.25 24615-20022.00 Melchers, Leo S. Meulenhoff, Elisabeth J.S. van Roekel, Jeroen S.C. Sela-Buurlage, Marianne B. Vloemans, Alexandra A. Woloshuk, Charles P. Cornelissen, Bernardus J.C. MBER: US/C8/047,413 19-APR-1993 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAM-1991
ATTORNEY/AGENT INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS SSEE: Morrison & Foerster :: 755 Page Mill Road Palo Alto California Sequence 10, Application US/08047413 Patent No. 5670706 29,959 REGISTRATION NUMBER: 29,956
REFERENCE/DOCKET UNMBER: 24
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-813-5600 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 1152 base pairs TYPE: nucleic acid STRANDEDNESS: single Murashige, Kate H CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19-APR-199 CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison
STREET: 755 Page Mil.
CITY: Palo Alto 94304-1018 CLASSIFICATION: 706141 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: SOFTWARE: US-08-047-413-10 NAME/KEY: APPLICANT: APPLICANT: COUNTRY: TELEX: STATE: Patent No. 722 782 737 g q δŏ a ŏλ ŏ 5 cgacagtggcgttcaagacggcgatatggttctggatgacgacgcagtccaacaagccgt 721

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                                                                Length 1152;
                                                            Score 316.8; DB 1; Length
Pred. No. 1.4e-53;
0; Mismatches 332; Indels
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Best Local Similarity 61.5%;
Matches 545; Conservative
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; LOCATION:
US-08-047-413-10
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Sequence 10, Application US/08229050 Patent No. 6066491

RESULT 12 US-08-229-050-10

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               Meichers, Leo S.
Meulenhoff, Elisabeth J.S.
Meulenhoff, Elisabeth J.S.
Sela-Buurlage, Marianne B.
Vloemans, Alexandra A.
Woloshuk, Charles P.
Bol, John F.
Linthorst, Hubertus J.M.
Linthorst, Hubertus J.M.
VENTION: FUNGAL RESISTANT PLANTS AND RECOMBINANT VENTION: POLYNUCLEOTIDES FOR USE THEREIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IN POCTA AND COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 316.8; DB 3;
Pred. No. 1.4e-53;
0; Mismatches 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-7AN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MALTASHIGE, Kate H.
REGISTRATION NUMBER: 29,959
REPRENCE/POCKET UNBER: 24615-20022.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-434-6792
Cornelissen, Bernardus J.C.
                                                                                                                                                                                                                                                                                              3: Morrison & Foerster 755 Page Mill Road
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INFORMATION FOR SEQ ID NO: 10:
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61.5%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 1152 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.5
Matches 545; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
                                                                                                                                                                                     TITLE OF INVENTION: F. TITLE OF INVENTION: O. TITLE OF INVENTION: P. NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                    STREET: 755 Page N
CITY: Palo Alto
STATE: California
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                                                                               APPLICANT:
APPLICANT:
APPLICANT:
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US-08-229-050-10
                   APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                APPLICANT:
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TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR

TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT

TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     721
                                       308 GATICIACAGITACAAIGCCIITAICAAIGCIGCIAGGICITITICCIGGCIITIGGIACIA 367
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ggttctacacgtacgacgccttcttggccgccggcggcgttcccggccttcggcacca
                                                                                                      GEGGIGATACCACTGCCCGTAAAAGAGAAATGCGGGCTTTCTTCGCCCAAACCTCCCATG
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Patent No. 6087560
GENERAL INFORMATION:
APPLICANT: Cornelissen, Bernardus J.C. APPLICANT: Melchers, Leo S. APPLICANT: Melchers, Leo S. APPLICANT: Wan Rockel, Elisabeth J.S. APPLICANT: Sela-Buurlage, Marianne B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Vloemans, Alexandra A. APPLICANT: Wolcshuk, Charles P. APPLICANT: Bol. John Charles P.
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Palo Alto
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COMPUTER: IBM PC compatible
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US-08-801-563-10
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCCTCGGCAGAACAATGTGGTTCGCAGGCGGGAGGTCCGCGTTGTGCCCTCGGGTCTCT 127
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 316.8; DB 3 Pred. No. 1.4e-53;
                                                                                                                                                                                 FILING DATE: 19-APR-1933
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTORNEY/AGBRY IRFORMATION:
NAME: MIRAShige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKEY NUMBER: 29,959
TELECOMMUNICATION: INFORMATION:
                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,413
                                                                      US/08/801,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.6%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 1152 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 545; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                               CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                 APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION:
US-08-801-563-10
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188 agagccagtgcactggctgcggtggcggc-----
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DNA (genomic)
                                                           27.18;
                                                                                            Conservative
                                                                             Best Local Similarity
 ) MOLECULE TYPE:
US-08-475-427-14
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US-07-842-165-14
                                                                                          Matches 505;
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                                                               Query Match
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APPLICANT: LEGIAX, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
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 508 CTIGIGGAAGAGCCATAGGAGIGGACCICCIAAACAAICCIGAITTAGIGGCCACAGAIC 667
                              662 cgacagtggcgttcaagacggcgatatggttctggatgacgacgccagtccaacaagccgt
                                                                                                                         728 CTTGCCACGATGTCATGGAAGATGGCAACCATCGTCTGCTGACGCGCGCAGCCAATC
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                                                                                              ogtgccatgacgtgatcacggggctgtggactccgacggccagggatagcgcagccggac
                                                  gggtacccgggtatggtgtcatcaccaacgtcatcaacggcgggatccaatgcggcatgg
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                                                                                                                                                                                                                     842 ggcagaacgacaaggtggcggatcggatcgggttctacaagcgctattgtgacattttcg
                                                                                                                                                                                                                                                                                 902 gcatcggctacgggaataacctcgactgctacaaccaattgtcgtt 947
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 16781/564/BEDL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Foley & Lardner
: 3000 K Street, N.W., Suite 500
Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/842,165
FILING DATE: 01.AMY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00607
FILING DATE: 21-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90 09460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/475,427 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08475427
Patent No. 5859340
GENERAL INFORMATION:
APPLICANT: DUBOIS, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 905 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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US-08-475-427-14
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                                                  Gaps
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Length 905;
Score 263.8; DB 2;
Pred. No. 2.6e-43;
0; Mismatches 317;
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470
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          APPLICANT: BUBGIS, Michel
APPLICANT: GRISON, Rene
APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: PIGNAD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
NUMBER OF SEQUENCES: 15
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                                                                                                                                                            SSEE: FOLEY & LARDNER
T: King Street Station, Sulte 500,1800 Diagonal
T: Road, FO Box 299
LEXANDRIA
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CHELCATION NUMBER: US/07/842,165
FILING DATE: 19920501
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 263.8; DB 2;
Pred. No. 2.6e-43;
0; Mismatches 317;
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                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY-AGENT INFORMATION:
NAME: SAXE, BERDARGIO D
REGISTRATION NUMBER: 28,665
REPERFORCE/OCKET NUMBER: 1678:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELER: 000140
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Best Local Similarity 59.9%;
Matches 505; Conservative C
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 905 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                               CORRESPONDENCE ADDRESS: ADDRESSEE: FOLEY & I
                                                                                                                                                                                                                              STATE: VIRGINIA
COUNTRY: USA
ZIP: 22313-0299
GENERAL INFORMATION:
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Search completed: May 3, 2002, 16:27:02 Job time: 7296 sec

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Sc02_08b0 HVSMEk000

HVSMEh009 HVSMEh009 HVSME1000 HVSMEh009

HVSME1002

HVSMEh008 ISC003.D0 HVSME1002

HVSME1000 HVSMEh009

HVSME1001 HVSMEC001 WHE313_F0 HVSME1000 WHE0327_A HVSME1001

HVSMED001

OM nucleic

on:

Sednence:

Title:

Searched:

Database

Result

No.

126429789112

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HV_CED0022E17f Hordeum vulgare seedling green leaf EST library HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone HV_CED0022E17f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Triticee; Hordeum.

1 (bases 1 to 816)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, X., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
                                                                                                                                                                                                                                                                                                                                                                                                                             BG366294 HVSME1000
BG907369 Talr1159E
BE602137 HVSMEh010
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BE405888 WHE0401_d
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                           BE425245 WHE313_A0
BG365634 HVSME1000
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BG367616 H
BG301220 F
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BG369588
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BF620099
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Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 792.
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AUTHORS
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COMMENT
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KEYWORDS
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BE405578 WHE1209_A
BE430003 TASO06.AO
BG253207 WHE2339_C
BG35535 HVSME1000
BE45557 HYSME1000
BE45557 HYSME1000
BE61746 HYSME1000
BE61746 HYSME001
BE602572 HYSME0100
BE602572 HYSME0100
                                                                                                                            (without alignments)
3395.224 Million cell updates/sec
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                               11351937 segs, 5372889281 residues
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Maximum Match 100%
Listing first 45 summaries
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BG365857
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09-MAR-2001

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605; Conserv
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KEYWORDS
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ORGANISM
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DEFINITION
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AUTHORS
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AL499683
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                                                                                      /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 291 c 282 g 121 t
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/clone="HV_EEEB0022E17f"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HVGDNAQNO5 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
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.1e-116;
les 71; I
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Pred. No. 2.1e-
0; Mismatches
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                                                                             /lab_host="SOLR"
                                                                                                                                                                                           70.5%;
91.1%;
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                     Local Similarity
nes 739; Conserv
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Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp."

233 c 228 g 98 t 1 others
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1; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute for Plant Genetics and Crop Plant Research Corrensstr.3, D-06466 Gatersleben, Germany Email: michalekeipk-gatersleben.de, http://pgrc.ipk-gatersleben.de Seq primer: Mi3rev primer for 3'end.

Location/Qualifiers
                                                                                                                                                Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 ggtcacgccggccacggccgagcagtgcggctcgcaagccggcggcgaccaagtgcgccga 122
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                                                                                                                     04-JAN-2001
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/lab_host="XLIBlue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctgcctgtgctgcagccagttcgggttctgcggcaccacctccgactactgcggcccccg
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                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 652)
Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Michalek W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                       AL499683 652 bp mRNA EST AL499683 Hordeum vulgare Barke etiolated leaves CDNA clone HK01K20r 3', mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 566.4; DB 1
Pred. No. 1.4e-94;
); Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Hordeum vulgare"
816
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/db_xref="taxon:4513"
/clone="HK01K20r"
ACCEGTACCCGGATACCGCGTGATCACCAAC
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NotI

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Tue May

us-09-534-229c-7.rst

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/note="Vector: pBluescript SK-; Site_1: Sall; Site_2: NotI : mRNA was made from etiolated leaves of spring barley variety 'Barke', a high quality malting variety. Plants were grown on filterpaper for 6 dat 25 C in the dark. Leaves were harvested at daylight conditions. Sal-Adaptor Sequence: TGACCAGGGGTGG Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window
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240 c 238 q 105 t 3 others
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                                                                                                                              542
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GGGGGACTTGGACCCGGAAGCGGGAGGTGGCCGCTTCTTCGGCCAGACTTCCACCAGA 360
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/clone_ilb="Hordeum vulgare Barke etiolated leaves"
/tissue_type="etiolated leaves"
/lab_horg="XLLBlue"
                                                                                                                                                                                                                              eggeaageagtaetatggeegeggeeceatecageteacecacacaactacaactacggaee
                                                                                                                                                                                                                                                                                  ggcgggccgcgcaatcggggtggacctgctgaacaatccggacctggtggccacggaccc
                                                                                                                                geaggageagggetegeegeegagetactgegaeeagagegeegaetggeegtgegeaee
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                                                                                                                                                                                                                                                                                                                                                                            Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.
EST sequencing and analysis in barley
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute for Plant Genetics and Crop Plant Research Corrensstr.3, D-06466 Gatersleben, Germany Email: michaleReipk-gatersleben.de, http://pgrc.ipk-gSeq primer: Ml3rev primer for 3'end.
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Pred. No. 1.4e-88;
0; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA clone HK06H20r 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
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AL500402.1 GI:12026638
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Local Similarity 91.6%;
les 597; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         693 bp
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Best Local S.
Matches 597,
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
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TITLE
JOURNAL
                   301
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AL500402
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Triticum aestivum

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 616)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wheat
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                                                                                                                                                                                                                                                                                                         CACCTACGACGCCTTCTTGGCCGCCGCCGCGCGTTCCCGGCCTTCGGTACCACGGGGGA 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson,O.D., Chaó,S., Choi,D.W., Close,T.J., Fenton,R.D., He
,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.L. and Tong,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 5105595773
Frax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE405578 616 bp mRNA EST 21-JUL-2000 WHE1209_A02_A03ZS Wheat etiolated seedling root cDNA library Triticum aestivum cDNA clone WHE1209_A02_A03, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ccgcgcaatcggggtggacctgctg-aacaatccggacctggtggc--cacggacccgac
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gccggccacggccgagcagtgcggctcgcaaqccggcggcgccaagtgcgccgactgcct
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                                 5 ecreeccareeceaecacaecaccecreecaecceeceececccaagreeccaacrecar
                                                                   gigetgeagecagticgggittetgeggeaceaecteegaetactgeggeeeeggtgeea
                                                                                        65 GTGCTGCAGCTACGGGTTCTGCGGCAGCACCTCCGCCTACTGCGGCGGCGGCTGCCA
                                                                                                                                             gagccagtgcactgggctgcggtggcggcggcggcggggggtggcctccatcgtgtccaggga
                                                                                                                                                                                                                                                                                       cacgtacgacgccttcttggccgccgccggcgttcccggccttcggcacaccggaga
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Anderson, O.D., Chao
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ORGANISM
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KEYWORDS
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quality sequence with phred score less than 20
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            Seq primer: Strategene SK primer.
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                     Location/Qualifiers
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91.2%;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooldeae; Triticaea; Triticum.

1 (bases 1 to 508)

S. Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Penillet,C., Gale,M., Graner,A., Gustufson,P., Harrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudlier,P., Eangridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Oqihara,Y., Pecchioni,N., Qualset,C., Schuch,M., Salvarij,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G. Silvarij,G., Shariflou,M., Expressed Sequence Tags for Species of the Triticeae

International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                   Streptophyta; Embryophyta; Tracheophyta; 
yta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canada
                                                                          BE430003 508 bp mRNA EST 26-JUL-2000 TASO06.A08R990616 ITEC TAS Wheat cDNA Library Triticum aestivum DB430003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cacgooggecacgaccgagcagtgcggctcgcaagccggcggcgaccaagtgcgactg 125
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/organism="friticum aestivum"

/db_xref="taxon:4165"

/clone="TAS006.A08"

/clone="TAS006.A08"

/clone="Inb="fric Tas Wheat cDNA Library"

188 c 175 g 79 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Gopalan.Selvaraj@nrc.ca
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 471.6; DB 10;
Pred. No. 3.2e-77;
0; Mismatches 9;
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ilarity 97.8%;
Conservative 0
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919
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Matches 499; Conserv
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG36536 805 bp mRNA EST 08-MAR-2001
HVSME10003B22f Hordeum vulgare 20 DAP spike EST library HVCDNA0010
(20 DAP) Hordeum vulgare CDNA clone HVSME10003B22f, mRNA sequence.
BG365536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Development of a genetically and physically anchored EST resource for barley genomics Unpublished (2000)
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggaagcgggaggtggcggccttcttcggccagacctctcacgagaccaccggcgggtggc 439
                                                                                                                                                       440 ccaccgcgcccgacggccccttctcatggggctactgcttcaagcaggagcagggctcgc 499
                                                                                                                                                                                                                                                                                                                                             241 CACCGAGCTACTGCGACCAGAGGGCGACTGGCCGTGCGCACCCGGCAAGCAGTACTATG 300
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                                                                                                                                                                                                                                          1 GGTTCCTGCTCCATCGCAACGACGCGCGTGCCTGGCCCGCGCGGTTCTACACGTACGACG
                                                                                                                                                                                                                                                                                                         500 cgccgagctactgcgaccagagcgccgactggccgtgcgcacccggcaagcagtactatg
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Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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BG365536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .480
// Organism="Triticum aestivum"
// Cultivar="Chinises Spring"
// Cultivar="Chinises Spring"
// Clone="WHE2339_C11_F21"
// Clone="WHE2339_C11_F21"
// Clone="Lib="Wheat pre-anthesis spike cDNA library"
// Lissue type="Spike before anthesis"
// dev_stage="Adult plant"
// Tab_host="E. coli SOLR"
// Iab_host="E. coli SOLR"
// Iab_host="E. coli SOLR"
// Site_1: EccNI: Site_2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 480)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han, P.S., Hais,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anglesis spike cDNA library
                                                                                                                                                                                                                                                                                                           BGZ65207 480 bp mRNA EST 16-FEB-2001 WHE2339_C11_F21ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE2339_C11_F21, mRNA sequence.
    caccggcgggtggcccaccgcgcccgacggccccttctcatggggctactgcttcaagca 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Strategene SK primer.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   800 Buchanan Street, Ālbany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                        479 AGAGCAGGCTTGGCCGTCGAACTACTGCGA 508
                                                                                                                                                                                 486 ggagcagggctcgccgccgagctactgcga 515
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                                                                                                                                                                                                                                                                                                                                                                                                                         BG263207.1 GI:12865133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 5105595818
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619 360

240

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/tissue_type="20 DAP spike"
/lab_host="Solk"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; For more details on library preparation and sequence analysis
                                                                                                                                                                                                                                                                                                                                                         EST library
                                                                                                                                                                                                                                                                                                                               /clone="HVSME10003B22f"
/clone_lib="Hordeum vulgare 20 DAP spike
HVcDNA0010 (20 DAP)"
clemson University Genomics Institute
Clemson University
100 Oordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                    /organism="Hordeum vulgare"/cultivar="Morex"
                                                                                                                                                      Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 778.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4513"
                                                                                                                               Email: rwing@clemson.edu
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VERSION KEYWORDS

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HVSMEG0017N15f Hordeum vulgare pre-anthesis spike EST library
HVCDNG008 (white to yellow anther) Hordeum vulgare cDNA clone
HVSMEG0017N15f, mRNA sequence.
see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 274 c 271 g 125 t
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                                                                                                                                                                                                                                                         74 CCGCATGTTGCTGCACCGCAACGGCGCCTGCCAGGCCAAGGGCTTCTACACCTACGA 133
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                                                                                                                                                                                                                           258 geggitectgetecategeaacgaegeagegigeetggeeegegggitetaeaegtaega 317
                                                                                                                                                              198 cactggetgcggtggcggcggcggcggggggggcctccatcgtgtccagggacctcttcga 257
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                                                                                                                               0;
                                                                                               Length
                                                                                                 DB 11;
                                                                                            Score 455.6; DB 11;
Pred. No. 2.9e-74;
0; Mismatches 179;
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/note="vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Iracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Hordeum.
1 (bases 1 to 584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST library
                                                                                                Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                     Development of a genetically and physically anchored EST resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                            for barley genomics
Unpublished (2000)
On Jul 26, 2000 this sequence version replaced gi:9465371.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="Morex"
/cultivar="Morex"
/dutivar="Morex"
/dutivar="Morex"
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/clone="HVSMEg0017N15f"
/clone="HVSMEg0017N15f"
/clone="Lib="Hordeum vulgare pre-anthesis spike"
/tissue_type="pre-anthesis spike"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@clemson.edu
seq primer: AATTAACCCTCACTAAGGG
High quality sequence stop: 567.
Location/Qualifiers
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/

QY g

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CIGGIGCGGCTCCACCTCGGACTACTGCGGCGACGGATGCCAGAGCCAGTGCTCCGGCTG 218
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BF619746.2 GI:13107773
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                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

7. Triticeae; Hordeum.

1. (bases 1 to 935)
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                                                                                                                                                                                                                                    HYSME10004109f Hordeum vilgare 20 DAP spike EST library HYCDAR0100 (20 DAP) Hordeum vilgare CDNA clone HVSME10004109f, mRNA sequence. BG365857
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        Gaps
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                                                                           aagcaggagcagggctcgccgccgagctactgcga-ccagagcgccgactggccgtgcgc
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HycDMs010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SoLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 Jordan Hall, Člemson, SC 29634, USA
Tel: 864 656 7288
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Clemson University Genomics Institute
Clemson University
                                                                                                                                          GCCCAGCAAGCAGTGCTTTGGCCCGGGCCCCATCC 583
                                                                                                                       540 acceggeaageagtactatggeegeggeeceatee 574
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/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 626.
Location/Oualifiers
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/clone="HVSMEi0004109f"
                                                                                                                                                                                                                                                                                                     BG365857.1 GI:13254956
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72.08;
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Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                      Hordeum vulgare
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Best Local Similarity
Matches 643; Conserv
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Butaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Butaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euraryota; Viridiceae; Pooideae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (bases 1 to 617)
Ming, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Mood, T.

Development of a genetically and physically anchored EST resource for barley genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       774 ageoggaegggt-accegggtatggtgteateaceaacgteateaaeggeggateeaat 832
                                                                                                                                                                 356
                                                                                                                                                                                                                     398
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                                                                                                                                                                                                                                                                                                              417 teaegagaceaceggegggtggeceacegegecegaeggecetteteatggggetaetg 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     578
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                                                 cgtgtccagggacctcttcgagcggttcctgctccatcgcaacgacgcagcgtgcctggc
                                                                                                                                                                                        caaggerittacaacatacgacgerttegregeegecgerategettege
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CGGCGGCGGCAGCACGCCCGTCACGCCCAACCCCATCGGGCGGCGGCGGCGTGTCCTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cttcaagcaggagcagggctcgccgagctactgcgaccagagcgccgactggccgtg
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603 ggcgggccgcgaat
                          GATAGGGCGGTCAAT
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AUTHORS
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                                                                                                                                                                                                                               485 aggagcagggctcgccgacgagctact--gcgaccagagcgccgactggccgtgcgcacc 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gggacctcttcgagoggttcottgctccatcgcaacgacgcagcgtgcctggcccgogggt 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        425 ccaccggcgggtggcccaccgcgcccgacggcccttctcatggggctactgcttcaagc 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 GCATGTGCTGCAGCCAGTTCGGGTTCTGCGGCAGCACCTCCGCCTACTGCGGCGCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 CCGCGCTGAGAGCACCTTGTGCGACGGCCATCCTGGTCGCCGTCCTGGCGGCGGCGGCGGCGGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 GCGACCTCTTCGAGCGGTTCCTCCTCCATCGCAACGACGCGGAGTGCCTGGGCCCCGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gagacctggacacgcggaagcgggaggtggcggccttcttcggccagacctctcacgaga
          On Dec 18, 2000 this sequence version replaced gi:11883480.
Contact: Wing RA
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 617;
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                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 422.4; DB 11;
Pred. No. 3.5e-68;
0; Mismatches 97;
                                      Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                     1. .617
/organism="Hordeum vulgare"
                                                               100 Jordan Hall, Clemson, SC 29634, Tel: 864 656 7288
Frax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 541.
Location/Qualifiers
                                                                                                                                                                                              /cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEc0009B09f"
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.6%;
Matches 514; Conservative
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Best Local Similarity
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Spermatophyta; Tracheophyta; Embryophyta; Tracheophyta; Traineophyta; Triticeae; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (bases I to 729)
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HycDNA0009 (5 to 45 DAP)"

/tissue_Lype="5-45 DAP Spike"
/lab_host="Solf"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; For
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BE602672 729 bp mRNA EST 02-MAR-2001
HVSNEh0101A21f Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare CDNA clone HVSMEh0101A21f,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
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Clemson University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SC 29634,
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Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="HVSMEh0101A21f"
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BE602672.1 GI:9860233
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Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                                                                                             mRNA sequence.
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6 g δy qq δ qq

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BG368852 623 bp mRNA BST 08-MAR-2001
VSWEL0020P03f Hordeum vilgare 20 DAP Spike EST library HVcDNR0010
(20 DAP) Hordeum vilgare CDNA clone HVSME10020P03f, mRNA sequence-
BG368852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
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Pred. No. 1.3e-66;
0; Mismatches 42
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91.3%;
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Matches 439; Conserv
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7 Triticeae; Triticum.

1 (bases 1 to 482)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat genomes - Normalized shoot cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE488961 482 bp mRNA EST 31-JUL-2000 WHE1077_C01_F01ZS Wheat unstressed seedling shoot normalized cDNA library Triticum aestivum cDNA clone WHE1077_C01_F01, mRNA
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/clone_lib="Wheat unstressed seedling shoot normalized
cDNA library"
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geceaecgegecegaeggecectteteatggggetaetgetteaageaggageaggggete 497
                                      276 GGCGACGGCACCGGACGGGGCCTTCGCCTGGGGCTACTGCTTCAAGCAGGAACGCGGCGC 335
                                                                                                                     336 CTCCICCGACTACTGCACCCCGAGGGCACAGAGTGGCCGTGCGCCCCCGGGAAGCGCTACTA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                   738 cacggggctgtggactccgacggccagggatagcgcagccggacgggtacccgggtatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  558 tggccgcggccccatccagctcacccaccaactacaactacggaccgggggccgcgcaat
                                                                                                                                                                                                                                                cggggtggacctgctgaacaatccggacctggtggccacggacccgacagtggcgttcaa
                                                                                                                                                                                                                                                                                                                                                                   516 GACGGCCATCTGGTTCTGGATGACGGCGCAGCCGCCCAAGCCGTCGAGCCATGCTGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 CGCCGGCCAGTGGAGCCCGTCAGGGGCTGACCGGGGCCGCAGGCGGGTGCCCGGGTTTGG
                                                                                498 geogeocgagetactgegaccagagegeogactggeogtgegeacceggeaageagtacta
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   696 CGCCGATCGAATC-GGITTIACAAGCGCIACIGIG 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 5105595773
Fax: 5105595818
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/note="Vector: Landad Uni-ZAP XR, excised phagemid phluescript SK; Site_1: BcoRL; Site_2: Xhol; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of callifornia, Riverside. The cDNA clones were in vivo excised to give phluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares'. Plasmid DNA protocol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preparations and DNA sequencing were performed in the Anderson lab (all other authors)." 170~c~161~g~83~t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eggitteetgeitegategeaaegaegeagegigeetggeeegegggitteiaeaegiaegae 318
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/tissue_type="Etiolated shoot"
/dev_stage="Five day old seedling"
/lab_host="E. coli DH10B"
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Similarity
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               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae, Pooldeae, Triticeae, Hordeum.
1. (bases 1 to 623)
                                                                                    Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
1 225 c 198 g 94 t l others
                                                                                                                                                        Development of a genetically and physically anchored EST resource for barley genomics
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 gggctactgcttcaagcaggagcagggctcgccgccgagctactgcgaccagagcgccga
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Pred. No. 9e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Bordeum vulgare 20
HycDNRO10 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SOLR"
                                                                                                                                                                                                                                                        Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                    Contact: Wing RA
Clemson University Genomics Institute
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/organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                            Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 585.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           /cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSME10020p03f"
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78.48;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               HVSME10004K07f Hordeum vulgare 20 DAP spike EST library HVcDNA0010 (20 DAP) Hordeum vulgare cDNA clone HVSME10004K07f, mRNA sequence. BG365887.1 GI:13254986
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Unpublished (2000)
                                                                                                                                                                             87 gtgcggctcgcaagccggcggcgccaagtgcgccgactgcctgtgctgcagccagttcgg 146
GGTGGCCACGGACCCGACCGTGTCGTTTAAGACTGCGATGTGGTTTTGGATGACGGCCCA 480
                                               708 gtccaacaagccgtcgtgccatgacgtgatcacggggctgtggactccgacggccaggga 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_zeri_axon:4513"
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/clone=lib="flordeum vulgare 20 DAP spike EST library
HVCDNA0010 (20 DAP)"
/tissue_type="20 DAP spike"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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High quality sequence stop: 888.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                               937 bp
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Hordeum vulgare
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/clone="WHEB131_A05.05"
/clone="Ib="Wheat unstressed seedling shoot cDNA library"
/tissue_type="Etholated shoot"
/dev_stage="Etholated shoot"
/dev_stage="Five day old seedling"
/dab_host="E. coli Solk"
/dab_host="E. coli Solk"
/note="Vector: Lambda Uni-Zap XR, excised phagemid;
/germinated and grown aspetically in the dark at room
/effotaxime in covered crystallization dishes. Shoots were
harvested. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the cDNA clones
were in vivo excised to give pBluescript phagemids in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."
                                Contact: Oith Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
West Area, Western Regional Research Center
West Area, Western Regional Research Center
Tel: 5105555773
Fax: 510555818
Email: candersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence have been trimmed score less than 20
Seq primer: Strategene SK primer.
Location/Qualifiers
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Pred. No. 1.2e-64;
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                                                                                                                                                                                                                                                                                                /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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90.48;
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                Unpublished (2000)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
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Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han P.S., Halala, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Iong, J.C.
The structure and function of the expressed portion of the wheat
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticum.

1 (bases 1 to 1985)
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Copyright (c) 1993 - 2000 Comp
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ABO48531 Psophocar M94106 Allium sati E13389 CDNA encodi E137876 Disum sativ S44869 basic chiti AF307511 Vigna ses

02-AUG-1996

Reisener, H.J. and Tiburzy, R. chitinase gene differentially

AUTHORS TITLE

SUMMARIES

175200 Sequence 9 L34210 Hordeum vul L00973 Zea mays ac Z29962 O.sativa (P D16222 Rice Cht-2 AB012855 Oryza sat AB018248 Oryza sat

AB051578 Secale ce D16221 Rice Cht-1 18465 Sequence 2 X56063 o.sativa m. X5437 Oryza sativ X87109 O.sativa RC Z29661 O.sativa RC Z29661 O.sativa RC L37289 Oryza sativ U02286 Oryza sativ AB051579 Secale ce M62904 H.vulgare L A37990 Sequence 9 AR037574 Sequence

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GSTSDYCGNCCQSQCNGCSGGGTPVPVPTPTGGGGVSSIISOSLFDQMLLHKNDAACQA
KGFYNYGAFVAAANSFSGFATTGGADVPKREVAAFLAQTSHETTGGMPTAPDGPFSWG
YCFNOERGAASDYCSPNSQMPCAPGKKYFGRGPIQISYNYN'CPAGRAIGTDLINNYD
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/organism="Triticum aestivum"
/outhivar="Chinese spring"
/db_xref="taxon:4565"
/clone_lib="lambda gem-12 genomic"
71. .1595
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precursor, mRNA, complete cds.
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Yeh.S., Moffatt,B., Griffith,M., Xiong,F., Yang,D.S.C.,
Wisemin,S.B., Sarhan,F., Danyluk,J., Xue,Y.Q., Hew,C.L.,
Doherty-Kirby,A. and Lajoie,G.
Chitinase genes responsive to cold encode antifreeze proteins
winter cereals
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/variety="Musketeer"
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FYNTGAFIDAANSFSAFATTGGTDVFKREVAAFLAQUISHETTGGWPTAPDGPYSWGYC
FNQBEGAPSDYCSPSQWPGAPGKYFGRGPIQISYNYNTGPAGRAIGTDLLANNPDLY
ATDATVSFKTALMFWTPQSPRPSSHDVITGFWSPSGADQAAGRVFGTYTINGG
LECGRGQDARVADRIGFYKRYCDLLGVSYGHNLDCYNQRPFA"
                                                                                     /protein_id="AAG53609.1"
/db_xref="G1:12407647"
/translation="MRGVVVVAMLAAAFAVSAHAEQCGSQAGGAICPNCLCCSKFGFC
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                                                  /codon_start=1
/product="31.7 kDa class I endochitinase-antifreeze
protein precursor"
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 chromosome="1"
                                   /note="cht9"
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Best Local Similarity 93.8
Matches 900; Conservative
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            sig_peptide
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Pred. No. 2e-105;
0; Mismatches 86;
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Du,M. and Ha,S.B.
Direct Submission submitted (22-APR-1997) Plant Biology,
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/strain="Glade"
/db_xref="taxon:4545"
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/gene="Chi3"
194. .346
/gene="Chi3"
/note="Chi1"
/codon_start=1
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Best Local Similarity 90.7%;
Matches 865; Conservative
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gcgaccacaggtagcaccgacgtcaagaagcgcgaggtggccgcgttcctcgctcagact
                                                         GGGACCACGGGCGCCACCGACGTCAGGAAGCGCGAGGTGGCCGCCTTCCTCGCTCAGACC
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Spermatophyta; Magnoliophyta; Liliopsida, Poales; Poaceae;
Pooideae; Poeae; Poa.
1 (bases 1 to 1080)
Du, M. and Ha, S.B.
Direct Submission
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Poa pratensis chitinase (Chi2) gene,
AF000966
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/strain="Glade"
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/product="chitinase"
/protein_id="AAF04454.1"
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28. .990
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/translation="MRGLVVVTILVAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFC
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CFKQEQGATSDYCSPSSQWPCAPGKKYFGRGPIQISYNYNYGPAGQAIQTDLLNNPDL
VLADFTVSFKTALWFWATAQSFKDSSRAVITGQWSPSSADQAAGRVPGYGVITNING
GLCCKGQDNRYAFKTAFYKRYCDLLGVSYGNNLDCYSQRPFGS"

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                                                                                                                                                                                      Length 1080;
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                                                                                                                                                                                    Score 796.6; DB 8;
Pred. No. 7.2e-105;
0; Mismatches 99;
xref="GI:6164588"
                                                                                                                                                                                       83.0%;
89.6%;
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta, Spermatophyta; Wagnoliophyta; Liliopsida; Poales; Poaceae, Ehrhartoideae; Oryzeae, Oryza, Losses 1 to 2808)
Nishizawa,Y., Kishimoto,N., Saito,A. and Hibi,T. Sequence variation, differential expression and chromosomal location of rice chitinase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (11-MAY-1993) to the DDBJ/EMBL/GenBank databases. Yoko
Nishizawa, National Institute of Agrobiological Resources, Rice
Genome Research Program: 2-1-2 Rannondai, Tsukuba, Ibaraki 305,
Japan (E-mail:CS.SUZUKI/NFRI, Tel:0298-38-7451, Fax:0298-38-7408)
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tgcttcaaccaggaggggggggggcactccgactactgcacgcggagtcgcagtggcca
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                                               gegaceacaggtageacegaegteaagaagegegaggtggeegegtteetegeteagaet
                                                                                                             421 teceaacgagacgaccggcgggtggccgacggcgcccgacggcccctactcctgggggctac
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VASNATVSFRTALWFWMTAQSPKPSSHAVITGQWSPSSADQAAGRVPGYGVITNIING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MRGLVVVAILVAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFC
GNTSDYCGTGCQSQCNGCSGPTPVTPPSGGGGVSSLVSQSLFEQMLLHRNDPSCQAN
GFYTYKAFTAAANSFAGFGTTGSTDVRKREVAAFLAQTSHETTGGWPTAPDGPYSWGY
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                     Pooldeae; Poeae; Poa.
1 (bases 1 to 1252)
Du,M. and Ha,S.B.
Direct Submission
Submitted (22-APR-1997) Plant Biology, U.C. Berkeley, Berkeley,
94706, USA
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                                                              CICCICGGCGICAGCIACGGAAACAACCIGGACTGCIACAGCCAGAGGCCGITCG
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Pred. No. 3.7e-102;
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(Chil) gene,
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                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Poa pratensis'
/strain="Glade"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="chitinase"
/protein_id="AAF04453.1"
/db_xref="G1:6164585"
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28. .1050
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AF000964
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28. .1050
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88.9%;
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VERSION
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/evidence=experimental
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/gene="Cit-3"
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/organism="Oryza sativa"
/strain="Nipponbare"
/db_xref="taxon:4530"
Submitted (11-MAY-1993) to DDBJ
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/codon_start=1
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L Submitted (23-MAY-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 27-12, Tsukuba, Daraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pleces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft' sequence."
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Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC clone: P0548E04
                                                                                                                                         2352 CCCAAGCCGGAGTGGCCGTGCGCCGCGCGCAAGAAGTACTACGGCCGGGGACCCATCCAG
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Oryza sativa
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                                                                                                                                                       Score 634; DB 2; Length 141534;
Pred. No. 1e-82;
                                                                                                 400 others
                                                                                                                                                                                      0; Mismatches 165; Indels
                                                                                                   μ
                                                                                    /clone="P0548E04"
29913 c 31342 g 40217

    141534
    Organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="6"

Location/Qualifiers
                                                                                                                                                          66.0%;
81.6%;
                                                                                                                                                          Query Match
Best Local Similarity 81.6
Matches 746; Conservative
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                                                                                                   39662
               source
                                                                                                   BASE COUNT
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STPYCGDGCQSQCSGCGGGSTPVTPTPSGGGGVSŠIVSRALFDRMLLHRNDGACQAKG
TYTDAFVBAASAFRGFGTTGGTDTRKREVAAFLAGUSHETTGGWATAPDGAFAWGYC
FKQERGATSNYCTPSAQWPCAPGKSYYGRGPIQLSHNYNGPAGRAIGVDLLRNDLV
AIDPFVSFKTAAMFWATAQAEKPSSHAVITGGWSPSGTDRAAGRVPGFGVIINIVNGG
IECGHGQDSRVADRIGFYKRYCDILGVGYGNNLDCYSQRPFA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MRAFVLFAVVAMAATMAVAEQCGSQAGGATCPNCLCCSRFGWCG
                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Bukaryota, Viridiplantae, Streptophyta, Embryophyta,

Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,

Pooldae, Triticeae, Hordeum.

1 (bases 1 to 1684)

Ignatius, S. M. J., Huang, J. and Muthukrishnan, S.

Isolation and characterization of a barley chitinase genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kansas State University,
66560, USA
19174 TACAAGCGCTACTGCGACATGCTGGGCGTCAGCTATGGCGATAACCTGGATTGCTACAAC 19115
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                                                                                                                                                                                                                                             30-MAY-1994
                                                                                                                                                                                                                                                                      Hordeum vulgare cultivar NK1558 chitinase gene, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muthukrishnan.S.
Direct Submission
Submitted (29-SEP-1993) Muthukrishnan S.,
Biochemistry, Willard Hall, Manhattan, KS
Location/Qualifiers
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Pred. No. 2.6e-81
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/product="chitinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="hydrolyzes chitin"
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/organism="Hordeum vulgare"
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/db_xref="taxon:4513"
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/db_xref="GI:495305"
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/clone_lib="lambda GT11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /EC_number="3.2.1.14"
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503. .509
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/product="chitinase"
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the DDBJ/EMBL/GenBank databases. Takeshi
                                                 2 (bases 1 to 1191)
Ohnuma.T., Yamagami,T. and Ishiguro,M.
Direct Submission
Submitted (22-NOV-2000) to the DDBJ/EMBL/GenBank databases. Take
Yamagami, Kyushu University, Protein Chemistry and Engineering,
Faculty of Agriculture; Hakozaki, 6-10-1, Fukuoka, Higashi-ku,
Fukuoka 812-8581, Japan (B-mail:Yamagami@uclink.berkeley.edu,
Tel:81-92-642-4218, Fax:81-92-642-3051)
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                of the Rye Seed
and Ishiguro, M.
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                                                                                                                                                                                                         1. 1191
/organism="Secale cereale"
/db_xref="taxon:4550"
                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB18519.1"
                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GI:11344587"
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  /product="seed
                                                                                                                                                                                                                                                                                                                                 /codon_start=1
Ohnuma, T., Yamagami, T. Cloning and Sequencing Unpublished
                                                                                                                                                                                                                                                                     /gene="rsca"
58. .1023
                                                                                                                                                                                                                                                                                                               /gene="rsca"
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                TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                  TITLE
JOURNAL
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Secale.
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DB 8; Length 1191;

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9 Gaps

231

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294 291 354 351 414 411 474

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(sites)

REFERENCE

DEFINITION

LOCUS

RESULT AB051578

ACCESSION

KEYWORDS VERSION

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ORGANISM

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GSTSAYGGSGCQGGGGGGTPPPGGGGSGVAGIVERDIANDACPA
KNEYTYDAFVAAANAPPSFATTGDAATRKRVAAFLAGISTSTATAGATAADGPS
YCFKEENNGWGSDYGGSGGGGGGGTPPSGGGGSGVAGIVERTTGGAATAADGPSWG
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                       initiation site"
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Pred. No. 5.2e-80;
0; Mismatches 190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="endochitinase"
687 c 665 g 67
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                                                            1318. .2289 7
/gene="Cht-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 64.7%;
Best Local Similarity 79.3%;
Matches 764; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chromosome 6.
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Best Local Similarity
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1 (bases 1 to 2739)
Nishizawa,Y., Kishimoto,N., Saito,A. and Hibi,T.
Sequence variation, differential expression and chromosomal location of rice chilinase genes
MOL. Gen. Genet. 241 (1-2), 1-10 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (sub_species japonica, strain Nipponbare) DNA, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (11-MAY-1993) to the DDBJ/EMBL/GenBank databases. Yoko Nishizawa, National Institiute of Agrobiological Resources, Rice Genome Research Program; 2-1-2 Kannondai, Tsukuba, Ibaraki 305, Japan (E-mail:CS.SUZOKI.NFRI, Tel:0298-38-7451, Fax:0298-38-7408) Submitted (11-MAY-1993) to DDBJ by:
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    cagtggccatgtgcgccgggcaagaagtacttcgggcgcggggcccatccagatctcacac
                                                                                                                                                                                                   715 CIGGIGGCCACGGACCCGACGGIGICGITIAAGACAGCCAIGIGGITIIGGAIGACGGCA
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                                                                                                                                                                                                                                                                                                                                                     aactacaactacgggccgggggagggcatcggcaccgacctgctcaacaacccggac
                                                                                                                                                                 cttgtggcgtcggacgcgaccgtgtcgtttaagacggcgttgtggttctggatgacgccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tactgcgacctccttggcgtcagctacggtgacaacctggactgctacaaccaaaggccg
                                      595 CAATGGCCGTGCCCCCAGGGAAGAGCTACTACGGCCGTGGGCCGATCCAGCTCTCCCAC
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1229. .1236
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Tsukuba, Ibaraki 305
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Nishizawa,Y.
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AUTHORS
TITLE
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TITLE
532
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REFERENCE
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SOURCE
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9 Gaps

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297

357

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237

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/organism="Oryza sativa"
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Zhu,Q. and Lamb,C.J.
Plant defense genes and plant defen
Patent: US 5695939-A 2 09-DEC-1997;
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Pred. No. 6.5
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartoideae; Oryzeae; Oryza.

1 (bases 1 to 1160)
Nishizawa,Y. and Hibi,T.
Isolation and characterization of a cDNA for rice chitinase Plant Sci. 76, 211-218 (1991)
2 (bases 1 to 1160)
Nishizawa,Y.
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Submitted (18-SEP-1990) Y. Nishizawa, NATIONAL INSTITUTE OF
AGROBIOLOGICAL RESOURCES, TSUKUBA SCIENCE CITY, KANNONDAI, IBARAKI
305, JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   476
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                                                                    CCGGGCCAGCAACTTCTACACCTACGACGCCTTCGTCGCCGCCGCCGCCGCCTTCCCGGG
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                                                                                                                                                                                                                                                          ctactgcttcaaccaggag---cgcggcgccacctccgactactgcacgccgagctcgca
                                                                                                                                                                                                                                                                                      534 giggocaigigcgccgggcaagaagtacticggggcgcggggccaiccagaictcacaca
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O.sativa mRNA for endochitinase.
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Oryza sativa
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/translation="MSTPRAASLAKKAALVALAAVLAAALATAARAEQCGAQAGGARC
PNCLCCSRWGWCGTTSDFCGDGCQSQCSGCGPTPTPPPSPSPSDGVGSIVPRDLFERLL
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IGVDLLSNPDLYATDATVSFKTALWFWMTPQGNKPSSHDVTTGFRAPSPADAAAGRAP
GYGVITNIVNGGLECGHGPDDRVANRIGFYQRYCGAFGIGTGGNLDCYNQRPFNSGSS
VGLAEQ"
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1 (bases 1 to 1186)
Nishizawa,Y., Kishimoto,N., Saito,A. and Hibi,T.
Sequence variation, differential expression and chromosomal location of rice chitinase genes
Mol. Gen. Genet. 241 (1-2), 1-10 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (13-NOV-1990) Y. Nishizawa, NATIONAL INSTITUTE OF
AGROBIOLOGICAL RESOURCES, TSUKUBA SCIENCE CITY, KANNONDAI, IBARAKI
                                                                                                                 781
                                                                                                                                                                                      841
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                                                662 GGATGACGCCGCAGTCGCCCAAGCCGTCGTGCCACGCGGTGATGACAGGGCAGTGGACGC
                                                                                  cetegggegeegaceaggeggegggggggggtgcetgggtacggtgtgatcaceaacatca
                                                                                                    teaacggtgggctcgagtgcgggcgcgggcaggacggccgtcgccgaccggatcgggt
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/db_xref="G1:407472"
/db_xref="SPTREMBL:Q43294"
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/organism="Oryza sativa"
/strain="japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
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/product="chitinase"
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/EC_number="3.2.1.14"
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/EC_number="3.2.1.14"
/product="chitinase"
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Nishizawa, Y.
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TTGDAATRKREVAAFLAQTGHETTGGWATAPDGPYSWGYCFKEENNGNVGSDYCVOSS
WPCDAGKKYYGRGPIQISYNYNYGPAGQAIGSNLLSNPDLVASDATVSFKTAFWFWM
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                                                                                                                                                                                       /translation="EQCGSQAGGALCPNCICCSQYGWCGSTSAYCGSGCQSQCSGSCG
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81.0%; Pred. No. 1.5e-78;
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                                                                                                                                 /protein_id="CAA39535.1"
/db_xref="G1:20202"
/db_xref="SPTREMBL:Q42993"
                                                                                                                                                                                                                                                                                                                                                                               186
/sub_species="japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                           13. .921
/EC_number="3.2.1.14"
/product="chitinase"
                                                                                  /EC_number="3.2.1.14"
                                                                                                 /codon_start=1/product="chitinase"
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                                                /clone="RCC1"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 1237)
                                                                                                                                                                                                                                                                                                                               Huang,J.K., Wen,L., Swegle,M., Tran,H.C., Thin,T.H., Naylor,H.M., Muthukrishnan,S. and Reeck,G.R. Nucleotide sequence of a rice genomic clone that encodes a class
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                                                                                                                                                                                                                                                                       Direct Submission
Submitted (25-AUG-1990) Wen L., Western Illinois University,
Department of Chemistry, Currens Hall, Macomb, IL 61455, USA
2 (bases 1 to 1237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cagagocagtgcaatggctgcagcggcggcaccccggtaccggtaccgacccctccggc
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                                                                             OSCHIT 1237 bp DNA PLA
Oryza sativa (rice) gene for endochitinase.
X54367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="L. Japonica"
/db_xref="taxon:4530"
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/clone_lib="EMBL3"
/clone="gilc2"
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/product="endochitinase"
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Oryza sativa
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                                                                                                                       DB 8;
                                                                                                                                                     206;
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      domain'
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                                                                                                                       Score 598.4; 1
Pred. No. 1.3e
0; Mismatches
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 /note="cysteine-rich di 1050. 1055 11057. 11052 11050. 1150 a 405 c 407 g
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77.9%;
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polyA_signal
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1 (bases 1 to 2048)

Xu,Y., Zhu,Q., Panbangred,W., Shirasu,K. and Lamb,C.
Regulation, expression and function of a new basic chitinase generation (Oryza sativa L.)

Plant Mol. Biol. 30 (3), 387-401 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIDS2/gggdata/geneseg/genesegn/Nal981.DAT:*
/SIDS2/gcgdata/geneseg/genesegn/Nal982.DAT:*
/SIDS2/gcgdata/geneseg/genesegn/Nal984.DAT:*
/SIDS2/gcgdata/geneseg/genesegn/Nal984.DAT:*
/SIDS2/gcgdata/geneseg/genesegn/Nal985.DAT:*
/SIDS2/gcgdata/geneseg/genesegn/Nal985.DAT:*
/SIDS2/gcgdata/geneseg/genesegn/Nal985.DAT:*
/SIDS2/gcgdata/geneseg/genesegn/Nal987.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               930621 seqs, 428662619 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Rye chitinase-like	RCH10 chitinase qe	Rice chitinase RCH	Nucleotide sequenc	cDNA encoding a ma	Sequence encoding	Floral organ-speci	Banana ripening fr	Sequence encoding	Chitinase coding's	Full length chitin
QI	AAX24889	AAQ31408	AAQ81346	AAF54983	AAA96224	AAQ62518	AAV49982	AAX25613	AAQ05264	AAT79940	AAT79941
DB	20	13	76	22	21	15	19	20	1	18	18
% Query Match Length DB	954	1151	1151	3035	1163	1002	1318	7397	4704	879	866
% Query Match	0.68	64.0	64.0	63.7	62.5	53.5	46.0	39.5	39.0	38.5	38.5
Score	854.6	614.6	614.6	611.4	600.2	513.6	441.4	379.2	374.4	369.2	369.2
Result No.	-1	7	e	4	Ŋ	9	7	89	σ	10	11

American elm chiti Tobacco intracellu	Nicotiana sp. intr	w	Banana fruit ripen	Banana fruit ripen		Banana fruit ripen	cDNA encoding a ma	Rye chitinase-like	encodin	Banana fruit ripen	Banana fruit ripen	\Box	Arabidopsis thalia		fruit I	Nettle lectin cDNA	Urtica dioica aggl	PR-Q cDNA cloned i	Tobacco PR-Q gene.	co PR-Q	PR-Q protein encod	PR-P cDNA cloned i	Tobacco PR-P gene	PR-P protein encod	Sequence encoding	nas	Sequence of chimer		tobacco e	Petunia extracellu	Petunia hybrida ex	cDNA sequence enco
AAT33325 AAQ12898	2	AAA58910	AAV69461	9	AAA96233	AAV69462	$^{\circ}$	6	AAA96234	9	Ø	AAA96230	AAC41918	æ	AAV69465	AAZ48613	AAC60211	AAQ06185	AAN90845	AAV62809	AAV72995	AAQ06186	AAV62813	AAV81601	AAQ21007	AAQ68352	AAQ21193	AAQ21191	AAQ74261	AAQ12897	AAT89951	90
17	18	21	20	20	21	20	21	20	21	20	20	21	21	19	20	21	22	ij	10	20	20	11	20	20	13	15	13	13	15	12	18	21
1225	1152	1152	721	755	1118	802	1013	756	583	768	169	1077	991	2636	730	1317	1317	1010	1020	1020	1020	896	968	968	1153	1153	1160	1863	1863	965	996	996
37.3	36.2	36.2	33.6	33.4	32.1	32.0	31.9	31.4	28.6	27.1	27.0	25.6	23.1	21.2	20.2	19.4	19.4	18.5	18.5	18.5	18.5	18.5	18.5	18.5	18.1	18.1	18.1	18.1	18.1	17.6	17.6	17.6
\sim		\sim	323	320.8	308.2	307	306			260		246	22.	03.	94.		86.	178	7	\sim	~	77.	77.	77.	73.	73.	73.	73.	73.	. 69		69.
12	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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CHT9; chitinase-like protein; antifreeze protein; AFP; winter rye; antifungal; fungicide; cold tolerance; frost tolerance; transgenic plant; preservation; cryopreservation; tumour; therapy;
                                                                                                                                                                 /*tag= a
/note= "separately claimed in Claim 2"
1..60
                                                                                                                                                                                           Rye chitinase-like protein CHT9 cDNA clone ch-9.
                                                                                                                                                Location/Qualifiers
1..954
                AAX24889 standard; cDNA; 954 BP
                                                                                                                                                                                                                                                                                          97US-0903872.
                                                   21-JUN-1999 (first entry)
                                                                                                                                Secale cereale
                                                                                                                                                                                                                                                                                           31-JUL-1997;
                                                                                                                                                                                                                                       W09906565-A2
                                                                                                                                                                                                                                                         11-FEB-1999.
                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                     mat_peptide
                                 AAX24889;
RESULT
AAX24889
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The present sequence encodes winter rye (Secale cereale L. cv. Maxateer) CHF9 preprotein (see AMW98079). Mature CHF9 (see AAW98080) is a chitinase-like protein that has chitinase (antifugal) and antificeeze activities. CHF9 DNA (ch-9) was obtained by isolating preprotein that has chitinase (antifugal) and change or other stresses, i.e. under conditions when only pathogens or other stresses, i.e. under conditions when only chitinases with antifreeze activity would be expressed, and then sorting the cold-induced chitinase CDNAs to determine which encoded proteins with ice-binding ability. CHF9 and CHF46 (see AAW9801-82) have been cloned and expressed in bacterial and yeast (Pichia) systems and in Arabidopsis thaliana. The chitinase-like antifreeze proteins can be used: to increase field survival of plants, animals and microorganisms to increase field survival of plants, animals and microorganisms to increase field survival of plants, animals and microorganisms spoosed to sub-zero temperatures; to inhibit ice recrystallisation and bypothermic protection of cells, embryos, tissues etc. (particularly human platelets); and to kill tumour cells. They are also used to inhibit initiation and progression of diseases or spoilage caused by low temperature pathogens

(particularly fungl) in plants, frozen foods and any cryopreserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 tteggtttetgeggeaceaeeteegaetaetgeggeaeeggetgeeagageeagtgeaat 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gagcaatgeggetegeaggeeggegggggegaegtgeeceaactgeetetgetgeageaag 120
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                                                                                                                                                    New nucleic acid encoding antifreeze polypeptides from plants -
particularly with chitinase activity, used to impart frost, and
pathogen, resistant to plants, for preservation of foods, cells etc.
and for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 atgagaggagttgtggtggtggccatgetggccgcggccttcgccgtgtctgcacacgcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 --ccgctgcggcggcacaccagtaccggtaccgacccccaccggcggcggcgtgtcctcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 954 BP; 162 A; 335 C; 306 G; 151 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.0%; Score 854.6; DB 20; 94.0%; Pred. No. 1.1e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                        Xiong
                                                                                                                                                                                                                                                       2; Fig 21a; 118pp; English.
                                                        щ
                                                        Moffatt
                                                                                                                 P-PSDB; AAW98079, AAW98080.
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                  BIOTECH INC
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                                                                                              WPI; 1999-153795/13
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Matches 900; Conserv
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                (ICEB-) ICE
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gggcgcgggcaggacggccgtgtcgccgaccggatcgggttctacaagcgctactgcgac 900
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teceacgagaccaccggcgggtggcccacggcgcccgacggcccctactcgtggggctac 477
                                                                                                                                 657
                                                                                                                                                                                                                     718 aaaccttcgagccacgacgtgatcacgggccggtggagccctcgggcgccgaccaggca 777
                                                                                                                                                                                                                                                     "Region conserved between class I and class II chitinases"
                                                                                                                      toggacgcgaccgtgtcgtttaagacggcgttgtggttctggatgacgccgcaatcaccc
                                                                                                                                                                                                                                                                                                   tgetteaaceaggagegegegeeceeteegaetaetgetegeegagetegeagtggeeg
                                                                  tgtgcgccgggcaagaagtacttcgggcgcggggcccatccagatctcacacaccaact
                                                                                                             tacgggccggcggggggggccatcggcaccgacctgctcaacaacccggaccttgtgggcg
                                                                                                                                                                            658 acggacgccaccgtgtcatttaagacggcactgtggttctggatgacgccgcagtcacca
                                                                                                                                                                                                  aagcettegageeacgaegtgateacgggeeggtggageeectegggegeegaegaggeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Promoter; region; rice; chitinase; physical; biological; stress; leaves; stems; roots; male; female; reporter; monocotyledon; dicotyledon; development; plant; defence; selectable; genes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/note=__Putative polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
55..1065
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/note= "Putative
                                                                                                                                                                                                                                                                                                                                                                                                               ВР
                                                                                                                                                                                                                                                                                                                                                                                                               AAQ31408 standard; DNA; 1151
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1053..1058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCH10 chitinase gene.
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 418
                                           478
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AAQ31408
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361 gegaceacaggtageacegaegteaagaagegegaggtggeegegtteetegeteagaet 420

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The sequence given represents the rice chitinase gene. The promoter region of this gene (see AAQ31407) is responsive to physical and/or biological stress. The pattern of expression of this gene in mature plants is characteristic. There is a low level of expression in leaves, a moderate level in plant stems and the highest level in roots and the male and female parts of the plant. The chitinase promoter sequence may be linked to a reporter gene for expression in mono- or dicotyladon plants. Expression of this reporter gene may be used to study patterns of development and controlled expression of plant defence genes and selectable genes.
                                                                                                                                                         DNA fragment contg. chitinase gene and its regulatory region responsive to mature plant stress and has low level expression leaves, moderate level expression in stem and high level
                                                                                                                                                                                                                                                           Disclosure; Page 33-34; 45pp; English
                 BIOLOGICAL STUDIES
                                                                                                WPI; 1992-415785/50
                                                                                                                                                                                                                     expression in roots
                 SALK INST
                                                                                                                   P-PSDB; AAR29019
                                                       Lamb CJ,
                 (SALK)
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1.S

Sequence 1151 BP; 197 A; 409 C; 353 G; 192 T; 0 other;

4, Gaps Length 1151; Indels Score 614.6; DB 13; Pred. No. 4.6e-101; 0; Mismatches 179; 0; 64.0%; ilarity 80.3%; Conservative Similarity Query Match Best Local S Matches 773

geogageagtgeggeageeaggeeggeggeggtgtgtgeeceaactgeetetgetgeage 174 55 atgagagegetegetgtggtggecatggtggecaggeeetteetegeggeggeggegtgeat 114 atgagaggagttgtggtggccatgctggccgcggcct---tcgccgtgtctgcgcac 57 115 g g ΩY QΣ

-aatggetgeageggeggeaceeeggtaeeggtaeegaeeeeeteeggeggeggegtete 236 aagtteggtttetgeggeaceaeeteegaetaetgeggeaeeggetgeeagageeagtge 1777 118

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octggccaaggggttctacaaactacggcgcttcgtcgccgccgccaactcgttctcggg ceeggecageaacttetacacctacgacgecttegtegecgecgecagegetteeeggg 297 351

410 416 470 476 530 533 590

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gacttcccacgagacgaccggcgggtggccgacggcgcccgacggccctactcctgggg 471 417

ctactgcttcaaccaggag---cgcggcgccacctccgactactgcacgccgagctcgca ctactgcttcaaggaggaggaacggcggcgggccggactactgccagcagagcgcgca 477

593 gtggccatgtgcgccgggcaagaagtacttcggggcgcggggcccatccagatctcacacaa

653 ctgcgacctccttggcgtcagctacggtgacaacctggactgctacaaccaaaggccgtt 953 594 ctacaactacgggccggcgggggggggcatcggcaccgacctgctcaacaacccggacct 651 etteaactaegggeeggeggggeaggeeateggegeegaeetgeteggegaeeet tgtggcgtcggacgcgaccgtgtcgtttaagacggcgttgtggttctggatgacgccgca atcacccaagccttcgagccacgacgtgatcacgggccggtggagcccttcgggcgccga 771 grogoccaagecgregtgeaacgeggregecaccggecagtggacgectecgecgacga ccaggoggogggagggtgcctgggtacggtgtgatcaccaacatcatcaacggtgggct cgagtgcggggcgggcaggacggccgtgtcgccgaccggatcgggttctacaagcgcta ggagtgcggccatggcgaggacgatcgcatcgccgaccggatcggcttctacaagcgcta BP. AAQ81346 standard; cDNA; 1151 ggc 1013 954 cgc 956 AAQ81346 714 831 891 951 894 RESULT AAQ81346 qq Ωÿ g δă 8 δŏ Db QΥ δŏ QQ δŽ pp

Chitinase; RCH10 gene; transgenic plant; disease resistance; crop improvement; tobacco; Nicotiana tabacum; plant defense; fungus pathogen; Cercospora nicotinae; (first entry) Rice chitinase RCH10 gene. Thanatephorus cucumeris; sativa 13-AUG-1995 Oryza

Location/Qualifiers 55..1065 94WO-US07815 15-JUL-1994; WO9502319-A 26-JAN-1995

STUDIES Maher EA, (SALK) SALK INST BIOLOGICAL Dixon RA, Lamb CJ, WPI; 1995-067090/09 P-PSDB; AAR67969 Transgenic plants contg. several plant defence associated proteins - have increased resistance to plant pathogens when grown in crops as a food source

Disclosure; Page 31-32; 45pp; English.

The SphI fragment of rice chitinase RCH10 gene (given in AAQ81346) and an alfalfa beta-1,3-glucanase coding sequence (AAQ81347) were

us-09-534-229c-8.rng

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transgenic tobacco, nicotinae and
                                                                                 Length 1151;
                                                                                                          11;
                                                                                                          Indels
                                             T; 0 other
                                                                                 DB 16;
                                                                                              .6e-101;
es 179;
incorporated into vectors for co-expression in resulting in improved resistance to Cercospora Thanatephorus cucumeris fungal infection.
                                                                                Score 614.6; E
Pred. No. 4.6e-
0; Mismatches
                                               BP; 197 A; 409 C; 353 G; 192
                                                                                 64.0%;
ilarity 80.3%;
Conservative
                                                                                               Similarity
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                                                                                  Query Match
Best Local Simi
Matches 773;
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                                                                                                                                                                                                                                         chitinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chineric plant receptors comprising a polynucleotide encoding a RRK receptor containing a heterologous extracellular domain and a kinase domain from a Xa21 polypeptide, useful for modulating plant responses
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Pred. No. 1.7e-100;
0; Mismatches 181; Indels 11;
                                                                                                                                                                                                                                        RKK gene; transgenic plant;
protein; RCH10 protein; ss.
                                                                                                                                                                                                             Nucleotide sequence of a rice chitinase designated RCH10
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80.1%;
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P-PSDB; AAB67444.
                                                                                                                                                                                                                                           Disease resistance
Xanthomonas; plant
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                                                                                                                              standard;
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The present sequence encodes a chitinase polypeptide. The specification describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896, AAB18895, and ABB1890-015), and glucosyl hydrolase family 18 chitinases (AAB18895, AAB18897-98 and AAB1890-01). The level of chitinase in plants can be modulated to enhance disease resistance in crop plants and for control of pathogens. The chitinase polynucleotides are also useful as molecular markers for genotype in a plant, and for sequence
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                          Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase famiy pathogen control; disease resistance; molecular marker; ss.
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cDNA encoding a maize chitinase polypeptide designated ZmCh7
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                                                                                                               Location/Qualifiers 32..817
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WPI; 1994-136599/17.
P-PSDB; AAR52577.
                                                                                 Eckes P, (Schellj,
                                09-OCT-1992;
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DE4234131-A.
                21-APR-1994
                                                                                Chet I, Mundy J,
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                                           gateteacacaactacaactacgggccggcggggggggcaggccatcggcaccgacctgctcaa
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                                                                                                                                                                                   686 caaccoggacctggtggccaccgacccaccgtgtcgttcgagaccgccgtctggttctg
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                 ggetteggeaccacggggggggcccgacgtgcagaagcgcgagctggcgcctggcggcgtt
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                                                                                  gccgagctcgcagtggccatgtgcgcgggcaagaagtacttcggggcgcgggcccatcca
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                                  cetegeteagaetteecaegagaegaecggeggtggeegaeggegeeeggaeggeeeeta
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/note= "Putative polyadenylation signal."
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  ggettegegaceacaggtageacegacgteaagaagegegag-
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/*tag= a
/product= Chitinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes Chitinase G. Chitinase is an enzyme which breaks down chitin, the major protein in insect exoskeletons. The coding sequence may be used in the construction of transgenic organisms, especially plants, to produce pathogen resistant organisms. The genome of such transgenic organisms preferably contains more than one gene with pathogen inhibiting activity, each gene under the control of active promoters. The two gene products then show a synergistic increase in pathogen induced activity so the transgenic organisms have a greater degree of resistance or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 acgacgcctgccaggccaaggcttctacacctacgacgccttcgtcgccgccgcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 513.6; DB 15; Length 1002;
Pred. No. 4e-83;
0; Mismatches 139; Indels 0;
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                                                                                                                            (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
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                                                                                                                                                                                      Sornhardt B, Goernhardt B;
                                                                                                                                                                                            Gornhardt
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Best Local Similarity 81.1%;
Matches 597; Conservative
92DE-4234131
                                                            92DE-4234131
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Gaps

54;

Indels

Length 1318;

19;

Score 441.4; DB 19 Pred. No. 2.6e-70; 0; Mismatches 231.

46.0%;

Best Local Similarity 70.6 Matches 684; Conservative

Query Match

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943
763
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                                                                                                  tgacgocgcaatcacccaagccttcgagccacgacgtgatcacgggccggtggagcccct
       acggcgggatcgagtgcggtcacgggcaggacagccgcgtcgccgatcgaatcgggtttt
                             acggtgggctcgagtgcgggggggggggacggacgtcgccgaccggatcgggttct
                                                                                          acaagcgctactgcgacctccttggcgtcagctacggtgacaacctggactgctacaacc
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This cDNA encodes a floral organ-specific chitinase. The specification provides a promoter sequence (AAV49983) derived from rice associated with chitinase, specific to floral organs that allows expression of genes in the flower parts of monocotyledonous plants. The expression of desired genes specifically in the floral parts of monocotyledonous plants, allows modifications to be made in the structure or function of these parts allowing the introduction of desired characteristics such as

Sequence 1318 BP; 231 A; 442 C; 440 G; 205 T; 0 other;

increased resistance to bacterial attack.

Promoter sequence associated with chitinase, specific to floral organs - allows expression of genes in the flower parts of

Claim 7; Pages 33-35; 67pp; Japanese.

monocotyledonous plants

WPI; 1998-388123/33. P-PSDB; AAW64776.

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5582 ccaegeceteccettecaetecegageggggggggganngttggetegateateateteet 5641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5581
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                                                                                                                                      Banana; fruit ripening; differential expression; fruit development;
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Pred. No. 2.8e-59;
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                                                                                                                                                                                                                                                                                                      (BOYC-) BOYCE THOMPSON INST PLANT RES.
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                                     AAX25613 standard; DNA; 7397 BP.
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63.9%;
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Sequence 879 BP; 216 A; 221 C; 242 G; 200 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                 Recombinant DNA contg. high level promoter and plant chitinase gene - for transforming plants to over:express chitinase, imparting resistance to phytopathogenic fungi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoding chitinase may be used to transform monoor dicotyledons to show increased resistance to fungal attack. A high level promoter is used from CMV 35s or 19s complement, NOS or CCS promoters of Agrobacterium opine synthetase gene, the RUBISCO small unit or the chlorophyl A/B binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 374.4; DB 11; Length
Pred. No. 2e-58;
0; Mismatches 281; Indels
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Similarity 65.6%;
                                                                                                                               88US-0285252
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                                                                                                                                                                                                                                                                    WPI; 1990-224529/29
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                                                                                                                                  16-DEC-1988;
WO9007001-A
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This sequence represents the coding sequence for the pumpkin chitinase. Chitinase is an enzyme decomposing chitin (not present in plant cell membranes) found in the cell membranes of fungi. Plants have this enzyme to protect themselves from pathogenic fungi. Thus this enzyme can be used to prevent plants from being infected with pathogenic fungi, and the chitinase gene can be introduced into plants to improve their resistance to diseases caused by fungi. As the amino acid sequence of the chitinase does not have any region to be cleaved by ubiquitous peptidases in cells, the chitinase produced by genetic recombination technology works for various host cells and serves for plant immunity to confer disease
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656 tggcgtcggacgcgaccgtgtcgtttaagacggcgttgtggttctggatgacgccgcaat
                                                                              2698 tegecactgaetetgteateteetteaagteegeeetetggttetggatgaeegeaegt
                                                                                                                                                                      cacccaagccttcgagccacgacgtgatcacgggccggtggagcccctcggggcgccgacc
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(SEKI-) ZH SEKIYU SANGYO KASSEIKA CENTER
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Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase; fungal cell membrane; pathogenic fungus; disease resistance; chitin; ss.

Location/Qualifiers 1..879 /*tag= a

pepo.

Cucurbita

Key

chitinase

/product= c

JP09163987-A.

Full length chitinase coding sequence.

(first entry)

13-OCT-1997

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   Length 879;
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                              Indels
   DB 18;
Score 369.2; DB 18;
Pred. No. 1.8e-57;
0; Mismatches 293;
38.5%;
Similarity 65.2%;
3; Conservative
                              583;
   Query Match
                   Local
                 Best Loca
Matches
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Chitinase derived from pumpkin - used to protect plants against

Claim 3; Page 4-5; 36pp; Japanese.

ZH SEKIYU SANGYO KASSEIKA CENTER

(NIHA) JAPAN ENERGY CORP

(SEKI-)

WPI; 1997-380170/35

P-PSDB; AAW24554

pathogenic fundi

95JP-0347367 95JP-0347367

14-DEC-1995; 14-DEC-1995;

24-JUN-1997

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Pred. No. 1.8e-57;
); Mismatches 293;
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BP.

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AAT79941; AAT79941

AAT79941 ID AAT7 XX AC AAT7 XX

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                                                                      tgetteaaceaggagegegeeaceteegaetaetgeaegeegagetegeagtggeea
                                                                                            tgcttcataagggag---agaaaccaagacgtatattgctcacctaaccagcaatggccg
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                                teccaegagaegaeggeggtggecgaeggegeeegaeggeeeetaeteetggggetae
                                                  346 teteatgaaaceaetggagggtgggetaeggeaeeggatggeeeatatgegtggggatat
                                                                                                                                                                                                                                                                                                                                                              Clone pHS2; chitinase; american elm; fungus; Ophiostoma ulmi; futch elm disease; E. coli; chitinase-like protein; fungal infection; ss.
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This sequence represents the CDNA clone pHS2, which encodes a protein having chitinase-activity derived from american elm. This protein inhibits the fungus Ophiostoma ulmi, the causative agent of dutch elm disease. The clone pHS2 may be used to transform E. coli cells for the recombinant production of the chitinase-like protein. The protein may be used in a composition to inhibit fungal infection of elm trees.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                actteccacqaqacqaccggcgggtggccgacggccccqacggcccctactcctggggc 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                              Isolated chitinase gene derived from an American elm - used to obtain prods. for inhibiting fungal infection of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1225 BP; 322 A; 277 C; 313 G; 313 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 358; DB 17;
Pred. No. 1.7e-55;
0; Mismatches 290;
                                                                                                                                                                                                                                           Claim 1; Fig 1; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          37.3%;
64.0%;
                              94US-0286020
                                                         94US-0286020
                                                                                      (UNMS ) UNIV MICHIGAN STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 64.0
Matches 575; Conservative
                                                                                                                     Sticklen MB;
                                                                                                                                                  WPI; 1996-353879/35
                                                                                                                                                                  P-PSDB; AAW00186
                            04-AUG-1994;
                                                         04-AUG-1994;
23-JUL-1996
                                                                                                                      Hajela RK,
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Best Local S
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0 other;

315 T;

273 C; 283 G;

281 A;

Sequence 1152 BP;

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tgcgggcggggcaggacggccgtgtcgccgaccggatcgggttctacaagcgctactgc 897
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                                                                                                                                                                                       gacctccttggcgtcagctacggtgacaacctggactgctacaaccaaaggccgttcg 955
                                           835 toggocogactacoggotacoggogtgatcaccaacattatcaacoggtgggatagaa
gcgtcggacgcgcaccgtgtcgtttaagacggcgttgtgtggttctggatgacgccgcaatca
                                                                                            geggegggaggtgeetgggtaeggtgtgateaecaacateateaaeggtgggetegag
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JF;
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/product= intracellular_chitinase
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Woloshuk
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10..984
                                                                                                                                                                                                                                                                                                                                                                    fungal resistance; phytopathogen;
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, Vloemans AA,
                                                                                                                                                                                                                                                                                                                                            intracellular chitinase
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RIJKSUNIV TE LEIDEN.
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P-PSDB; AAR13275.
                                                                                                                                                                                                                                                                       AAQ12898 standard;
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Sela-Buurlage MB,
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  1152;
                      24;
  Length
                       Indels
  12;
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                       0; Mismatches
Score 347.6;
Pred. No. 1.2
36.2%;
illarity 63.2%;
Conservative
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 Query Match
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                                                                                                                       caacgacgcggcgtgcctggccaaggggttctacaactacggcgccttcgtcgccgccgc
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10..984
/*tag= a
         183 ttgccagagccagtgccctggtggtccca-
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                                                                                                                                                                       Intracellular chitinase; antifungal; transgenic plant; synergism; beta-1,3-glucanase gene; tobacco; ss.
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63.2%; Pred. No. 1.2e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fungus-resistant transgenic plants - containing genes intracellular chitinase and beta-1,3-glucanase
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                                                                                                                                  Nicotiana sp. intracellular chitinase cDNA
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                         CDNA; 1152
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                                                                                                                                                                                                                                                                                                                                                                                                         specification describes transgenic plants which express a chitinase gene and a glucanase gene. The expression of the chitinase and beta-1,3-glucanase genes produces an antifungal effect. The transgenic plants are useful for improving plant resistance to pathogenic fungi. The recombinant polynuclectides and the process are useful for producing fungal resistant plants.
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Melchers LS, Meulenhoff EJS, Sela-buurlage MB; oshuk CP, Bol JF, Linthorst HJM, Van Roekel JSC;

Woloshuk CP,

Cornelissen BJC,

Vloemans AA,

WPI; 2000-498214/44. P-PSDB; AAB07513.

93US-0047413. 97US-0801563

18-FEB-1997;

US6087560-A sig_peptide

11-JUL-2000

19-APR-1993;

(UYLE-) RIJKSUNIV LEIDEN. (MOGE-) MOGEN INT NV.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to construct a transgenic plant in a novel method to produce plants resistant to fungal attack. Such transgenic plants expressing an intracellular plant chitinase gene and a plant beta-1,3-glucanase gene within its tissues are predicted to exhibit improved resistance to pathogenic fungi. Such genes should be operably linked to promoters and terminators and optionally a gene encoding a selectable or screenable trait. Plants that overexpress the chitinase and glucanase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cetetgetgeageaagtteggtttetgeggeaceaceteegaetaetgeggeacegge-- 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This CDNA sequence encodes an intracellular chitinase which is used
                                                                                                                      antifungal; transgenic plant; synergism; tobacco; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 347.6; DB 18; Length 1152; Pred. No. 1.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.2e-53;
0; Mismatches 314; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ĽS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sungus-resistant transgenic plants - containing genes intracellular chitinase and beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1152 BP; 281 A; 273 C; 283 G; 315 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Melchers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Linthorst HJM, Melcher
1ge MB, Van ROEKEL JSC;
                                                                                                                                                                                                                                             /*tag= b
y-.981
/*tag= c
/product= intracellular_chitinase
                                                                                             Nicotiana sp. intracellular chitinase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exhibit a synergistic antifungal effect.
                                                                                                                                                                                       Location/Qualifiers
10..984
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S, Sela-buurlage MB,
Woloshuk CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Fig 2; 42pp; English.
               1152
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63.2%;
                                                                                                                                                                                                                                                                                                                                                                  93US-0047413,
                                                                                                                                                                                                                                                                                                                                                                                             91US-0647831.
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                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     MOGEN INT NV.
RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                CDNA;
                                                                                                                      chitinase;
                                                                                                                                    beta-1,3-glucanase gene;
                                                                                                                                                                                                                               10..78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-479536/44.
P-PSDB; AAW31297.
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                standard;
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                                                                                                                      Intracellular
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Best Local Simil
Matches 580; C
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                                                                   11-MAR-1998
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Meulenhoff
               AAT89952
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The present sequence encodes an extracellular chitinase. The specification describes transgenic plants which express a chitinase gene and a glucanase gene. The expression of the chitinase and beta-1,3-glucanase genes produces an antifungal effect. The transgenic plants are useful for improving plant resistance to pathogenic fungi. The recombinant polynuclectides and the process are useful for producing fungal resistant plants.
                                                                                                                                                                                                                                                                                                                                                    improved
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                                                                                                                                                                                                                                                                                                                                             New transgenic plants expressing chitinase and glucanase have improveresistance against pathogenic fungi, particularly against Alternaria alternata or Fusarium oxysporum f. sp. lycopersici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                      Melchers LS, Meulenhoff EJS, Sela-buurlage MB;
oshuk CP, Bol JF, Linthorst HJM, Van Roekel JS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 tggtggggatctcggcagtatcatctcaagttccatgtttgatcagatgcttaagcatcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 347.6; DB 21; Length 1152; Pred. No. 1.2e-53;
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/product= "chitinase"
10..78
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63.2%;
                                                                                                                                 97US-0801563,
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91US-0647831.
                                                                                                                                                                                                                                                                    Woloshuk CP,
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Matches 580; Conservative
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                                                                                                                                                              19-APR-1993;
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                           sig_peptide
                                                                      US6087560-A
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Sequence 14, 3
Sequence 14, 3
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Sequence 15, Sequence 15,
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Sequence 1,
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GenCore version 4.5
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US-08-449-315-7
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Maximum Match 100%
Listing first 45 summaries
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Sequence 2, Application US/07704288C
Patent No. 5399680
GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, GUN
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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COUNTRY: United States
2 IP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: DS/07/704,288C
FILING DATE: 2-MAY-1991
CLASSIPICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: RELECT. Stephen E.
REGISTRATION NUMBER: 31,192
REFERRNCE/DOCKET NUMBER: P31 8899
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFERX: (619) 546-4737
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Pred. No. 1.6e-112;
0; Mismatches 179;
US-08-455-736-7
US-08-971-217-7
US-08-181-2718-12
US-08-444-803-12
US-08-444-803-12
US-08-444-913-12
US-08-456-265A-12
US-08-455-2416-12
US-08-455-416-12
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US-08-455-244-12
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US-08-456-240-12
US-08-456-240-12
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US-08-9350-600-12
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CORRESPONDENCE ADDRESS:
ADDRESSEB: PRETTY, SCHROEDER, BRUEGGEMANN &
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CITY: Los Angeles
STATE: California
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                                             175 CAGTICGGCTGGTGCGGCTCCACCTCCGACTACTGCGGCGCCGGATGCCAGAGCCAGTGC
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Sequence 1, Application US/08093372

RESULT 2 US-08-093-372-1

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                                                                                                             PLANTS CONTAINING MULTIPLE
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Pred. No. 1.6e-112;
0; Mismatches 179;
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                                                                                                                                                                                   E: Pretty, Schroeder, Brueggemann & 444 South Flower Street, Suite 2000
Patent No. 5530187
GENBRAL INFORMATION:
APPLICANT: Lamb, Christopher J.
APPLICANT: Lamb, Qun
APPLICANT: Maher, Eileen A.
APPLICANT: Maher, Eileen A.
TITLE OF INVENTION: TRANSGENIC PLANTS CONTAIN
TITLE OF INVENTION: DISBASE RESISTANCE GENES
NUMBER OF SEQUENCES: 4
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11: 800
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                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31,192 REFERENCE/DOCKET NUMBER: P4 TELECOMMUNICATION INFORMATION: 619-546-4737
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Best Local Similarity 80.3%;
Matches 773; Conservative (
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LENGTH: 1151 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       619-546-9392
                                                                                                                                                                                                                                         STATE: CA
COUNTRY: U.S.A.
ZIP: 90071-2921
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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US-08-093-372-1
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                                                                                                                                                                                                    STREET: 444 South
CITY: Los Angeles
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                                                                  REFERENCE/DOCKET NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 86
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 546-4737
TELEFAX: (619) 546-9392
TELEX:
                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                               64.0%;
80.3%;
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1151 base pairs
TYPE: nucleic acid
STRANDEDNES: unknown
TOPDLOGY: unknown
MOLECULE TYPE: DNA (genomic
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            APPLICATION NUMBER: US 0° FILING DATE: 22-MX-1991
ATTORNEY/AGENT INFORMATION: NAME: Relier, Stephen E. REGISTRATION NUMBER: 31,
                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 80.3
Matches 773; Conservative
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
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; LOCATION: 55..1062
US-08-379-259-2
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                 cttcgcgaccacaggtagcaccgacgtcaagaagcgcgaggtggccgcggttcctcgctca
                                                                          gacttoccacgacgaccggcgggtggccgacggcgcccgacggcccctactcctgggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: 05/08/379,259 FILING DATE:
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Patent No. 569593
GENERAL INPORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: DEFENSE GBI;
TITLE OF INVENTION: DEFENSE REGULATO!;
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                Gaps
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                                                                11;
   Length 1151;
                                                          Indels
Score 614.6; DB 1;
Pred. No. 1.6e-112;
0; Mismatches 179;
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Matches 597; Conservative
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LOCATION: 298..312
OTHER INFORMATION: /nc
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LOCATION: 349..378
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LOCATION: 466..588
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LOCATION: 133..861
              OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
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                                                                                                                               CCAGCGGGCCGGCCGCGGCCTACGGCGTCATCACCAACATCATCAACGGCGGGCT
                                                                                                                                                                        834 cgagtgcgggcgcgggcaggacggccgtgtcgccgaccggatcgggttctacaagcgcta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic pathogen-resistant organism 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Graves, Donohue and Raymond
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/function= "chitinase"
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FILING DATE: June 1, 1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 18,839
REGISTRATION NUMBER: 35,225
REFERNEK/POCKET NUMBER: A29542 FWC -
TELEPHONE: (212) 408-2500
TELEPHONE: (212) 408-2500
MULTELEPHONE: (212) 765-2519
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STREET: 30 Rockefeller Plaza
CITY: New York
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
ILENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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LOCATION: 64..861
OTHER INFORMATION:
OTHER INFORMATION:
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TITLE OF INVENTION:
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LOCATION: 1..63
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/product= "26 kD preprotein of chitinase G (ChiG)"
/hote= "antifungal activity, especially on
Trichoderma reesil and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
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signal"
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COCATION: 607..86
CHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
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OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "probable signal peptide
sequence"
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                                                                                                                                                                                  FEATURE:
NAME/KEY: 3'UTR
LOCATION: 862.1002
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3'
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81.1%;
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NAME/KEY: polyA_signal
LOCATION: 905..910
OTHER INFORMATION: /note
OTHER INFORMATION: signa
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LOCATION: 64..294
OTHER INFORMATION: /not
OTHER INFORMATION: sequ
FEATURE:
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NAME/KEY: sig_peptide
LOCATION: 466..58
LOCATION: 466..58
CHERR INFORMATION: sequence"
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Best Local Similarity 81.1%;
Matches 597; Conservative
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NAME/KEY: sig_peptide
LOCATION: 298.312
OTHER INFORMATION: /not
OTHER INFORMATION: sequ
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133..861
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                                                         LOCATION: 64.861
OTHER INFORMATION:
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OTHER INFORMATION:
5'UTR
1..63
              LOCATION:
FEATURE:
NAME/KEY:
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US-08-812-025-9
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                                                                                                                                                                                                                  668 cagegergaccagecegeaegecegergecegerrreergrearcaccaacarcarca 727
                                                                                                                        704 tgaegeegeaateaceeaageettegageeaegaegtgateaegggeeggtggageeeet
                                                                                                                                            teteacacaactacaactacgggcggggggggggggcaggccatcggcaccgacctgctcaaca
                   TCTCCCACAACTACAACTATGGACCTGCCGGCCGGGCCATCGGGGTCGATCTGCTGGCCA
                                                               acccggaccttgtggcgtcggacgcgaccgtgtcgtttaagacggcgttgtggttctgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic pathogen-resistant organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPARE: PATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRINA APPLICATION DARA:
APPLICATION NUMBER: US/08/812,025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond STREET: 30 Rockefeller Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08812025
; Patent No. 5804184
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Transgenic pai
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kole, Lisa
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: A28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 408-2500
TELEFAX: (212) 765-2519
TELEX: 23855
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 18,839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                           aaaggccgttcgcata 959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: cDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10112 D.S.A.
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FEATURE:
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US-08-812-025-9
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/codon_start= 64
/function= "chitinase"
/function= "26 kD preprotein of chitinase G (ChiG)"
/note= "antifungal activity, especially on
Trichoderma reesii and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
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LOCATION: 905..910
OCHER INFORMATION: /note= "potential polyadenylation
OTHER INFORMATION: signal"
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OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
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LOCATION: 607..86
CHIBR INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
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sequence"
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                                                                                                                                                                           NAME/KEY: 3'UTR
LOCATION: 862.1002
OTHER INFORMATION: /mort= "11 nucleotides at 3'
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Pred. No. 9.5e-93;
0; Mismatches 139;
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FEATURE:
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704 tgacgccgcaatcacccaagccttcgagccacgacgtgatcacgggccggtggagccct 763
                                                                                                                    584 totcacacaactacaactacggggggggggggggggcatcggcaccgacctgctcaaca
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09138873A Patent No. 6271438 GENERAL INFORMATION:
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STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Tenser, Arthur REGISTRATION NUMBER: 18,839
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REGISTRATION NUMBER: 35,225
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TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEG ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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: New York
RY: U.S.A.
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STATE: New YO
COUNTRY: U.S
TO: 10112
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US-09-138-873A-9
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/function= "chitinase"
/function= "26 kD preprotein of chitinase G (ChiG)"
/product= "antifungal activity, especially on
Trichoderma reesil and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
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OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3' end not shown"
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Pred. No. 9.5e-93;
0; Mismatches 139; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "potential polyadenylation
signal"
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sequence"
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OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
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sequence"
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sequence"
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81.1%;
                                   MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Hordeum vulgare
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NAME/KEY: sig_peptide
LOCATION: S66.588
OTHER INFORMATION: Anot
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NAME/KEY: sig_peptide
LOCATION: 298.312
OTHER INFORMATION: /not
OTHER INFORMATION: sequ
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LOCATION: 905..910
OTHER INFORMATION: /not
OTHER INFORMATION: sign
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Best Local Similarity 81.1
Matches 597; Conservative
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607..861
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LOCATION: 64..294
OTHER INFORMATION: /nc
OTHER INFORMATION: sec
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LOCATION: 349..378
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FEATURE:
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                   linear
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STRANDEDNESS:
TOPOLOGY: lin
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LOCATION:
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US-09-138-873A-9
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248 CCGCCTTCCCGGGCTTCGGCACCACCGGCAGCGCCGACGCCCAGAAGCGCGCGAGGTGGCCG
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APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela
TITLE OF INVENTION: A Chitinase cDNA Clone From a
TITLE OF INVENTION: Disease Resistant American
TITLE OF INVENTION: Elm Tree
NUMBER OF SEQUENCES: 1
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ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
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OPERATING SYSTEM: MS-DOS 5.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Okemos
STATE: Michigan
COUNTRY: USA
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238 tecattatetegeagtegetettegaceagatgetgetgeacegeaacgaegeggegtge 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 aagttoggtttetgeggeaceaecteegaetaetgeggeaeeggetgeeagageeagtge 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 aatggetgeageggeggeaceceggtaecegtaecegaececetecggeggeggegtetee 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 GGTCTCATATCAAGCTCCGCCTTTAATGACATGCTTAAGCATCGTAACGACGGTGGTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 358; DB 1; Length 1225; Pred. No. 3e-62; . 0; Mismatches 290; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD: sequencing OTHER INPORMATION: DNA needed for chitinase OTHER INFORMATION: in elm.
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 GGCGCCAGCGTAGCGAT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: NAME/KEY: chitinase encoding DNA
NAME: IAN C. MCLEOd
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4103
TELERX: (517) 347-4103
TELERX: No. 5539056
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Ulmus Americana
STRAIN: NPS 3-487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 37.3%;
Best Local Similarity 64.0%;
Matches 575; Conservative (
                                                                                                                                                                                                             SEQUENCE COLLEGE LENGTH: 1225
TYPE: Nucleic Acid STRANDEDNESS: Single TOPOLOGY: Linear MOLECULE TYPE: DNA
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DEVELOPMENTAL STAGE:
HAPLOTYPE: N/A
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POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE: N/P
CELL TYPE: N/A
CELL LINE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                        655 AACTATGGACAGTGGGAAGGGCCATAGGAGCAAACCTATTAAACAACCTGGTCTCGTA 714
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535 TACTGCTACAATAGGGAGCAAAACCCTTCTTCCGATTATTGTTCTTTTAGTCCTACTTGG 594
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                                                                ccatgtgcgccgggcaagaagtacttcgggcgcgggcccatccagatctcacacaactac
                                                                                                                   CCITGING CONTROL CONTRO
                                                                                                                                                                                                                                                                                                                            gogteggaegegaeegtgtegtttaagaeggegttgtggttettggatgaegeegeaatea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 48864
COMPUTER REABALE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage COMPUTER: Acer
COMPUTER: Acer
MEDIUM SYSTEM: MS-DOS 5.00
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-603-919-1; Sequence 1, Application US/08603919; Patent No. 5728382
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TELECOMMUNICATION:
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(517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: NO. 5728382e
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ian C. McLeod
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Nucleic Acid STRANDEDNESS: Sing]
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APPLICANT: Masome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tactgottcaaccaggagcgcgcgccccccgactactgcacgccgagctcgcagtgg 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aactaogggccggcgggggggcatcggcaccgacctgctcaacaacccggaccttgtg 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACTATGGACAGTGTGGAAGGGCCATAGGAGCAAACCTATTAAACAACCCTGATCTCGTA 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 aatggetgeageggegeeceeggtaceggtacegaeceeceeteeggeggeggegtetee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 358; DB 1; Length 1225;
Pred. No. 3e-62;
0; Mismatches 290; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION METHOD: sequencing OTHER INFORMATION: DNA needed for chitinase OTHER INFORMATION: in elm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: chitinase encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.3%;
64.0%;
                                                                                                                                              Ulmus Americana
                                                                                                                                                                                                                                                                                                                                                                        N/A
N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; PUBLICATION INFORMATION:
US-08-603-919-1
                                                                                                                                                               STRAIN: NPS 3-487
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE: N
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Best Local Similarity
                                                                                                                                                                                                                                                    N/A
                                                                                                                                                                                                                                                                                                        N/A
                             S.
                                                       ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                 HAPLOTYPE: N/
TISSUE TYPE:
CELL TYPE: N/
CELL LINE: N/
MOLECULE TYPE:
                             HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                               ORGANELLE:
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Gaps

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                                                                          cgtgtetgegeaegeegageaatgeggetegeaggeeggegggggggegaegtg
                                                                                                                                                      cctctgctgcagcaagttcggtttctgcggcaccacctccgactactgcggcaccggc--
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                                       24;
 Length 943;
                                       Indels
Score 349.2; DB 2;
Pred. No. 1.6e-60;
); Mismatches 313;
                                                                                                                                                                                                                                                          132 TIGCCAGAGCCAGTGCCCTGGTGGTCCA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 15, Application US/07842165
; Patent No. 5932698
                                       0;
36.4%;
Similarity 63.3%;
31; Conservative
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US-07-842-165-15
                                     581;
   Query Match
                       Local
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APPLICANT: DEGRAY, Jean-Jacques
APPLICANT: DEGRAY, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
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                                                                          834
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                                                                                                                                     835 TCGGCCGGCCGACTGCGGCCTACGCCGTGATCACCATTATCAACGTGGGATAGAA 894
 GCAACTGACCCTGTCATTTCCTTCAAAACGGCCTTATGGTTCTGGATGACCCCACAGTCA 774
                                                                                                                                                                                        tgegggegegggeaggaeggeegtgtegeegaeeggateggggttetaeaagegetaetge 897
                                                                                                                                                                                                             955 GATATCCTTAGAGTTGGCTATGGGAACAATCTTGATTGCTATAACCAGAGGCCTTTTG 1012
                                                                                                                                                                                                                                                                898 gacctccttggcgtcagctacggtgacaacctggactacaaccaaaggccgttcg 955
                                                                                                           778 goggogggggggggggcctgggtacggtgtgatcaccaacatcatcacggtgggctcgag
                                                            CCAAAGCCCTCGTGCCATGACGTCATCACCGGAAGATGGAGTCCTTCCGGCACCGACCAG
                                       cocaagccttcgagccacgacgtgatcacgggccggtggagccctcgggcgccgaccag
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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: 3000 K Street, N.W., Suite 500
Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO PCT/FR91/00607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/842,165
FILING DATE: 01-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/475,427
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO PCT/FR91, FILING DATE: 21-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90 09460
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08475427
Patent No. 5859340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (202)672-5300
(202)672-5399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 943 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
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APPLICANT: Bol, John F. APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR TITLE OF INVENTION: OPTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
 351 GGCTTTCTTCGCCCAAACCTCCCATGAACTACAGGAGGATGGGCAACAGCACCAGATGG 410
                                                                                                                                                            471 ACCAAGTGGTCAGTGGCCTTGTGCTCCTGGTCGGAATATTTCGGAGGCCCCATCCA 530
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                                                                                                                                                                                                                                                                                   caaccoggaccttgtggcgtcggacgcgaccgtgtcgtttaagacggcgttgtggttctg 701
                                                                                                                                                                                                                                                                                                                      591 CAATCCTGATTTAGTGGCCACAGATCCAGTAATCTCATTCAAGTCAGCTCTCTGGTTTTG 650
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                                                                                                                                                                                                                                 cecetaetectgggggetaetggtteaaceaggagegegegeeaeeteegaetaetgeae
                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE: 19-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cornelissen, Bernardus J.C.
Malchers, Leo S.
Meulenhoff, Elisabeth J.S.
van Roekel, Jeroen S.C.
Sela-Buurlage, Marianne B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vloemans, Alexandra A. Woloshuk, Charles P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08047413 Patent No. 5670706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
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MEDIUM TYPE: Floppy disk
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CITY: Palo Alto
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                                                                                 APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
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                                                                                                                                                                                                      STREET: King Street Station, Suite 500, 1800 Diagonal STREET: Road, PO Box 299
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/842,165
FILING DATE: 19920501
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 349.2; DB 2;
Pred. No. 1.6e-60;
0; Mismatches 313;
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                                   GRISON, Rene
LEGUAY, Jean-Jacques
PIGNARD, Annie
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
                                                                                                                                                                                      ADDRESSEE: FOLEY & LARDNER
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63.38;
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(703) 683-4109
                 Michel
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INFORMATION FOR SEQ ID NO: SEQUENCE CRARACTERISTICS: LENGTH: 943 base pairs TYPE: NUCLEIC ALLD
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Best Local Similarity 63.3
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                                                                                                                                                                                                                                         CITY: ALEXANDRIA STATE: VIRGINIA
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OPERATING SYSTEM:
                                 GRISON,
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SENERAL INFORMATION:
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APPLICANT: Bol, John F.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
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822 caacggtgggctcgagtgcggggcgcgggacggacggccgtgtcgccgaccggatcgggtt
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                                                                                                                                                                                                                                                                                                                                          882 ctacaagcgctactgcgacctccttggcgtcaggctacggtgacaacctggactgctacaa
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Melchers, Leo S.
Meulenhoff, Elisabeth J.S.
van Roekel, Parcen S.C.
Sela-Buurlage, Marianne B.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Vloemans, Alexandra A. APPLICANT: Woloshuk, Charles P. APPLICANT: Bol, John F. APPLICANT: Linthorst, Hubertus J.M. APPLICANT: Linthorst, Hubertus J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08229050 Patent No. 6066491 GENERAL INFORMATION:
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755 Page Mill Road
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SEQUENCE CHARACTERISTICS:
LENGTH: 1152 base pairs
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CORRESPONDENCE ADDRESS:
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STATE: California
COUNTRY: USA
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TELEFAX: 412
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US-08-229-050-10
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Pred. No. 3.3e-60;
0; Mismatches 314;
                                                                                                                                                                                                               24615-20022.00
                PRICE APPLICATION DATE:
APPLICATION NUMBER: US 07/647,831
PILING DATE: 29-784-1991
ATTOMEY AGENT INFORMATION:
NAME: MULTASHIGGEN RATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-2002;
TELECHONE: 415-494-0792
                                                                                                                                                                                                                                                                                                                                      TELEX: 706141
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 63.2%;
Matches 580; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 1152 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION:
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US-08-047-413-10
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                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
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US-08-801-563-10
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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 RESULT 13
US-08-801-563-10
                                                                                  APPLICANT:
APPLICANT:
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                                                                                    24;
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                                                     Score 347.6; DB 3;
Pred. No. 3.3e-60;
0; Mismatches 314;
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US-08-229-050-10
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 TCTCTGCTGCAGCAATTTGGTTGGTGTGGTAACACCAATGACTATTGTGGCCCTGGCAA 182
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Pred. No. 3.3e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFRAX: A15-813-5600
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                                                                    Cornelissen, Bernardus J.C
                                                                                       Melchers, Leo S.
Meulenhoff, Elisabeth J.S.
van Roekel, Jeroen S.C.
                                                                                                                                                       Sela-Buurlage, Marianne B.
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29-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/801,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 Vloemans, Alexandra A. Woloshuk, Charles P.
; Sequence 10, Application US/08801563; Patent No. 6087560; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        Morrison & Foerster
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTAL. ZIP: 94304-1018

ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
CANGER: 1152 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-APR-1993
APPLICATION NUMBER: US 07//
FILING DATE: 29-TAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MUTAShige, KEL E.
REGISTRATION NUMBER: 29,95:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.2%;
63.2%;
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APPLICATION NUMBER: US
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EDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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STATE: California
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                                                MEDIUM TYEE: KIOPPY GIRK
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRHY APPLICATION DATA:
APPLICATION NUMBER: US/08/475,427
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/842,165
FILING DATE: 01-MAY-1992
PRIOR APPLICATION NUMBER: WO PCT/FR91/00607
FILING DATE: 21-JUL-1991
PRIOR APPLICATION NUMBER: FR 90 09460
FILING DATE: 24-JUL-1990
ATTORNEY/AGBNT IMPORMATION:
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Pred. No. 7.4e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 16781/564/BEDL. TELECOMMUNICATION INFORMATION:
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60.6%;
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                                       Floppy disk
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LENGTH: 905 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
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Matches 516; Conservative
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                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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MOLECULE TYPE:

US-08-475-427-14
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                                       eggeggeggegtetectecattatetegeagtegetettegaceagatgetgetgeaceg
                                                                               22 IGGIGGGGATCTCGGCAGTATCATCTCAAGTTCCATGTTTGATCAGATGCTTAAGCATG
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Patent No. 589340
GENERAL INFORMATION:
APPLICANT: DUBOIS, Michel
APPLICANT: GRISON, Rene
APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: POPPAN, Alain
183 TIGCCAGAGCCAGIGCCCIGGIGGICCCA
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                                               Length
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                                                                               324;
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                                              Score 289.6; DB 2
Pred. No. 7.4e-49;
); Mismatches 324
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Job time: 7325 sec
JS-07-842-165-14
                                                                     Best Local Sim
Matches 516;
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                                                                                                                   cggaccttgtgggggtcggacgcggtgtcgtttaagacggcgttgtggttctggatga 706
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cacacaactacaactacgggccgggggggggggcatcggcaccgacctgctcaacaacc
                                                                                   CACACAACTACAACTATGGGCCATGTGGAAGAGCCCATCGGAGTGGACCTTTTAAACAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GRISON, Renardacques
APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a print of prevention; having endochitinase activity correspondence address: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/07/842,16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIR: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/07842165
Patent No. 5932698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: SARE, Bernhard D
FRGISTRATION NUMBER: 28,665
REFERENCE/POCKET NUMBER: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 905 Dasse pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US
FILING DATE: 19920501
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US-07-842-165-14
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WHE0982_G HVSME1000

HVSME1002 HVSMEh009

PI1_65_E1 Zm06_01a0 HVSME1000 HVSMEh009

BG415203 H BG368854 H BG3668854 H BE500345 W BE500345 M AL499683 A AL499683 A AL499683 A BE500112 W BE500112 W BE500112 W BE50012 W BE500335 H BG36512 H BG36512 H BG36514 H BG36514 H BG36514 H BE60254 H BE63650 D BG83610 BG83610 BG83610 BG83610 BG83610 BG83610 BG83610 BG83610 BG83610 BG83611 BE602137 H BE602578 BG83611 BE6036511 BE6036511 BG836510 BG836510 BG836510 BG836510 BG836510 BG836510 BG836510 BG836510 BG836510 BE6036511 BG836510 BE6036511 BG836512 BG8365

AL500402 HVSMEh009 Zm06_09b0 Zm06_02b0

Searched:

Database

Result Š.

Sequence:

Run on:

PII 65 E1 Zm06 01a1 707094C01 Zm06 05f0 HVSME1000 HVSMED008

WHE1209_A HVSMEh010

Zm06 06e0 HVSME1001 HVSMED001

HVSME1000 HVSME1000 HVSMEh009

WHE2054_D HVSMEh008

HVSME1002

WHE0978_E

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Hordeim vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                              Triticeae, Hordeum.

1 (bases 1 to 705)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
                                                                                                                                                                                                                                                                                                                              BG367460 705 bp mRNA EST 08-MAR-2001
HVSWE10012F13f Hordeum vulgare 20 DAP spike EST library HVCDNA0010
(20 DAP) Hordeum vulgare cDNA clone HVSWE10012F13f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Development of a genetically and physically anchored BST resource for barley genomics
Unpublished (2000)
Contact: Wing RA
Clemson University
Colemson University
100 Jordan Hall. Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 705
/organism="Hordeum vulgare"
/cultivar="Morex"
                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 690.
                                                                                                                                                                 BG836200
BG836379
                      BE500345
BG366386
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BE454845
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BG366294
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BG301220
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AL499683
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AUTHORS
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BG365536 HVSME1000
BG365857 HVSME1000
BF064981 HV_CED002
BE602672 HVSME1000
BG365887 HVSME1000
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3353.307 Million cell updates/sec
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BG368852 E
BG414551 E
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                                                         3, 2002, 16:24:10 ; Search time 3076.35 Seconds
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         4.5
Compugen Ltd.
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                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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          GenCore version
Copyright (c) 1993 - 2000
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BE705117
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BG368852
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BE602672
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                                          OM nucleic - nucleic search, using sw model
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1 (bases 1 to 711)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu. X., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and Wood,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 260 c 224 g 109 t
                                                                                                                            Development of a genetically and physically anchored EST resource
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                                                                                                                                          for barley genomics
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 572.8; DB 1 Pred. No. 1.2e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Hordeum vulgare
HVcDNA0010 (20 DAP)"
/tissue_type="20 DAP spike"
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                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hordeum vulgare"
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                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="Morex"
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/clone="HVSMEi0012P08f"
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                                                                                                                                                                                                                                                                                                                                High quality sequence stop: (
Location/Qualifiers
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94.5%;
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Wing, R.
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                                   REFERENCE
AUTHORS
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                                                                                   /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/parley/ To order a clone see http://www.genome.clemson.edu/orders" 261 c 219 g 108 t
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HYSME10012P08f Hordeum vulgare 20 DAP spike EST library HYCDNA0010
(20 DAP) Hordeum vulgare cDNA clone HYSME10012P08f, MRNA sequence.
BG367616
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Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                     Score 578.4; DB 1.
Pred. No. 1.1e-98;
0; Mismatches 31
             /clone_lib="Hordeum vulgare 20
HycDMNO100 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SolR"
/clone="HVSMEi0012F13f"
                                                                                                                                                                                                                                       60.28;
94.78;
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AUTHORS
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COMMENT
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//dev_stage="seedling three-leaf stage"
//note="Vector: Bluescript SK+/Xhol-EcoRI; Site_1: Eco RI;
//stage.stage.stage seedling trated for one week at 20C, 12 hrs light/day. Library made with
Stratagene UNIZAP XR Kit/(not packaged). cDNA is directly
ligated into SK+/Xhol-EcoRI, then electroporated into
// 10Plo cells (livitrogen). It is others
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                                                                                                                                                                                                                                                                                                                                            Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="Puma (winter rye)"
/b_xref="taxon.4550"
/clone="sc02_08b02"
/clone_lib="Sc02_AAFC_ECORC_cold_stressed_winter_rye_seedl
                                                                                                                                                                                                                                                                                                                                                                                                             Hattori
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooid Titiceae; Secale.

( Dases 1 to 681)
Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Hatt, J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A.
Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings Unpublished (2000)
                                                                                                                                                                                                                          BE705117 681 bp mRNA EST 12-SEP-2000 SC02_08b02_A SC02_AAFC_ECORC_cold_stressed_winter_rye_seedlings Sco2_ale cereale cDNA clone Sc02_08b02, mRNA sequence. BE705117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Singh,J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
960 Carling Avenue, Bldg. 20, Ottawa, Ontario, KIA 0C6, Canada
Tel: (613) 759-1662
Pax: (613) 759-1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cogcaacgacgcggcgtgcctggccaaggggttctacaactacggcgccttcgtcgccgc 338
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ctactgettcaaaccaggagegegegecaeeteegaetaetgeaegeegagetegeagtg
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; Pred. No. 9.6e-97;
13; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Secale cereale"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="leaf, crown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               singhja@em.agr.ca.
Location/Qualifiers
                                                                                                                                                                                                                                                                                    BE705117.1 GI:10093382
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JOURNAL
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Triticeae; Hordeum.

1 (bases 1 to 805)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu. Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae
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/cultivar="Morex"
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Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 778.
Location/Qualifiers
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Tel: 864 656 7288
Fax: 864 656 4293
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Unpublished (2000)
Contact: Wing RA
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Hordeum vulgare
Bikaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triliceae; Hordeum.
1 (bases 1 to 935)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo Wood,T.
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HVcDNA0010 (20 DAP)"
HYCDNA0010 (20 DAP)"
/Lissue_type="20 DAP spike"
/lab_bost="Sold"
/
HVSWEI0004109f Hordeum vulgare 20 DAP spike EST library HVCDNA0010 (20 DAP) Hordeum vulgare CDNA clone HVSME10004109f, mRNA sequence. BG365857
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Unpublished (2000)
Contact: Whors RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
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Pred. No. 2e-81;
0; Mismatches 200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality semmenon
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/clone="HVSMEi0004109f"
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Local Similarity 76.5%;
Les 687; Conservative
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                                                                                                              /note="vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To coder a clone see http://www.genome.clemson.edu/orders" 274 c _ 271 g _ 125 t
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HVcDNA0010 (20 DAP)"
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           /clone="HVSMEi0003B22f"
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,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
; Triticeae; Hordeum.
1 (Dases 1 to 816)
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                                               ccatgtgcgccgggcaagaagtacttcgggcgcgggcccatccagatctcacacaactac
                                                                                                                                                                       574 cogrececceaeceaecaacaecracraceccerececcearccaecreceaecrac
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/cultivar="CI16151 (Mla6)"
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Seq primer: AATHAACCCTAAAGGG
High quality sequence stop: 792.
Location/Qualifiers
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                                      /clone_1hp="Hordeum vulgare seedling green leaf EST /clone_lib="Hordeum vulgare seedling green leaf EST library HycDNA0005 (Erysiphe infected & control)" /tissue_type="seedling green leaf" /lab_host="Soura" /nab_host="Soura" /note="Vector: lambdaZAP; Site_1: EcoRl; Site_2: Xhote="Vector: lambdaZAP; Site_1: EcoRl; Site_2: All S
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pred. No. 1.9e-76;
0; Mismatches 166;
/db_xref="taxon:4513"
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75.8%;
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/db_xref="moutes" |
/db_xref="taxon:4513"
/db_xref="taxon:4513"
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/clone_lib="Hordeum vulgare 20 DAP spike EST library
/tissue_type="20 DAP spike"
/tab_host="Sola"
/nab_host="Sola"
/note="Vector: lambdaZAP; Site_l: EcoRl; Site_2: Xhol; For more details on library preparation and sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (bases 1 to 937)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG365887 937 bp mRNA EST 08-MAR-2001
HVSME10004K07f Hordeum vulgare 20 DAP spike EST library HVCDNA0010
CO DAP) Hordeum vulgare cDNA clone HVSME10004K07f, mRNA sequence.
BG365887 GI:13254986
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Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                          595
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                                                                                                                                                                                                                                                                         accoggacettgtggcgtcggacgcgaccgtgtcgtttaagacggcgttgtggttctgga 703
                                                                                                                                                                                                                                                                                                                                                                                     tgacgccgcaatcacccaagccttcgagccacgacgtgatcacgggccggtggagcccct 763
CCITCGCCIGGGGCIACTGCTICAAGCAGGAACGCGCCGCCTCCTCCGACIACTGCACCC 355
                                                    824 acggtgggctcgagtgcggggcgggcaggacggcgtgtcgccgaccggatcgggttct
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Seq primer: AATTAACCCTAAAGGG
High quality sequence stop: 888.
Location/Qualifiers
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Fax: 864 656 4293
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Wood,T.
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Hordeum vulgare

Hordeum vulgare

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Wagnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

; Triticeae; Hordeum.
                                                                                                                    BE602672 729 bp mRNA EST 02-MAR-2001
HVSMEh0101A21f Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0101A21f,
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 729)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y.
X., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Development of a genetically and physically anchored EST resource for barley genomics for barley genomics for Dipublished (2000) Contact: Wing RA Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             403
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Pred. No. 3.1e-76;
0; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 713.
Location/Qualifiers
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80.98;
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                                                                                                                                                                                                            mRNA sequence.
BE602672
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Pred. No. 2.3e-75;
0; Mismatches 164; Indels
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/tissue_type="20 DAP spike"
/lab_host="SOLR"
/lab_host="Yector: lambdaAAP; Site_1: EcoRl; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/Darley/ To order a clone see http://www.genome.clemson.edu/orders"
a 259 c 240 g 121 t lothers
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Prodeum.
1 (bases 1 to 742)
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                                                                         Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
                                                                                                                                              Development of a genetically and physically anchored EST resource for barley genomics Unpublished (2000)
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Pred. No. 1.2e-72;
0; Mismatches 116;
                                                                                                                                                                                                                                                                       SC 29634, USA
                                                                                                                                                                                                           Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="HVSMEi0003102f"
/clone_lib="Hordeum vulgare
HVcDNA0010 (20 DAP)"
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                              Email: rwing@clemson.edu
Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 707.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Morex"
/db_xref="taxon:4513"
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al Similarity 81.4%;
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539 ACCCGGACCTGGTGGCCACGGACGCCACTGTGGCGTTTAAGACGCCCATCTGGTTCTGGA 598

BG365634 742 bp mRNA EST 08-MAR-2001 HVSME10003102f Hordeum vulgare 20 DAP spike EST library HVcDNA0010 (20 DAP) Hordeum vulgare cDNA clone HVSME10003102f, mRNA sequence.

GI:13254733

BG365634.1

BG365534

ACCESSION

VERSION KEYWORDS

DEFINITION

BG365634

COCUS

Hordeum vulgare

ORGANISM

SOURCE

barley.

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BG368854
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
Triticaes 1 to 908)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
'Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
'T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG415203 908 bp mRNA EST 13-MAR-2001
HVSMEk0005116f Hordeum vulgare testa/pericarp EST library
HVcDNA0013 (normal) Hordeum vulgare cDNA clone HVSMEk0005116f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Contact: Wing RA
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                                                                                                                                                                                                          435 cggcgggtggccgacggcccgacggccctactcctggggctactgcttcaaccagga 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
547 ACCCGGACCTGGTGGCCACGGCCACTGTGGCGTTTAAGACGGCCATCTGGA
                                                                                             TGACGGCGCAACCGCCCAAGCCGTGGAGCGTGCTGTGATCGCCGGCCAGTGGACCCCGT
                                                            tgacgccgcaatcacccaagccttcgagccacgacgtgatcacgggccggtggagcccct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
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Bmail: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAGGG
High quality sequence stop: 815.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       acggtgggctcgagtgcgggcgcgggcagg 853
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BG415203.1 GT:13320754
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Matches 484; Conservative C
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BG415203
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
Thitocae; Hordeum.
Hoases 1 to 625
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu.,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
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HVSMEi0020P07f Hordeum vulgare 20 DAP spike EST library HVCDNA0010
(20 DAP) Hordeum vulgare cDNA clone HVSMEi0020P07f, mRNA sequence.
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Contact: Wing RA
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                                                                gogogogocacctccgactactgcacgccgagctcgcagtggccatgtgogccgggcaa
                                                                                                                                                                                                                                                                                                                                          gtegtttaagaeggegttgtggttetggatgaegeegeaateaeceaageettegageea
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Seq primer: AATTAACCCTCACTAAAGGG
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                               REFERENCE
                                           AUTHORS
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                                                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 223 c 202 g 93 t lothers
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Hordeum vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                         235 tectecattatetegeagtegetettegaceagatgetgetgeacegeaacgaegeggeg 294
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                                                                                                                                                                                                                                                                                                                                                              GGCTTCGGCACCACCGGCGGAACCGACCCGGAAGCGCGGAGGTGGCCGCCTTCCTGGCC 181
/clone_lib="Hordeum vulgare 20 DAP spike EST library HVCDNA0101 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SolR"
                                                                                                                                                                                                  Gaps
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ri
                                                                                                                                                                      Length 625;
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                                                                                                                                                                   Score 420.6; DB 11;
Pred. No. 3.2e-69;
); Mismatches 120; I
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                              Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 312 c 280 g 181 t 2 others
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                                                                                                                                                                                         Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
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                                                                                                                                                                                                            for barley genomics
Unpublished (2000)
On Jul 26, 2000 this sequence version replaced gi:9462873.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4293
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Pred. No. 2.2e-68;
0; Mismatches 150; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 616.
Location/Qualifiers
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/clone="HVSMEh0093N17f"
                            Hordeum.
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Best Local Similarity 77.0%;
Matches 535; Conservative
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I (bases 1 to 969)
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